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OM protein - protein search, using sw model

Run on: September 20, 2001, 16:14:27 ; Search time 20.83 seconds (without alignments)

Sequence: US-09-525-885-2 ; 1 MASAMASVQILOREVFKKWI.....KLVRITPGEQWGLFTAKM 494

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2204	84	8	Environmental stre
2	206.5	7.9	285	A. halophila sarco
3	204.5	7.9	317	Synechocystis gamm
4	198	7.6	283	Spm1 protein invol
5	193.5	7.4	279	E. halochloris sar
6	189.5	7.3	275	S. lavendulae Mit
7	189.5	7.3	283	S. lavendulae Mit
8	188	7.2	293	Arabidopsis thalia
9	188	7.2	296	Arabidopsis thalia
10	188	7.2	336	Arabidopsis thalia
11	188	7.2	339	Arabidopsis thalia

RESULT. 1

ID AAB80627 standard: Protein; 473 AA.

XX AAB80627;

XX DT 02-MAY-2001 (first entry)

DE Environmental stress tolerant protein SEQ ID 40.

XX KW Environmental stress resistance; salt; heat; desert; transgenic plant.

XX OS Sueada Japonica.

XX PN WO200106006 A1.

XX PD 25-JAN-2001.

XX PF 19-JUL-2000; 2000W0-JP04862.

XX PR 19-JUL-1999; 99JP-0235910.

PR 24-MAR-2000; 2000JP-0085377.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Yamada A, Ozeki Y, Saito T;

XX DR WPI; 2001-147355/15.

DR N-PSDB; AA74206.

XX PT Screening method to obtain DNA encoding environmental stress resistance

PT factor, useful for producing transgenic plants resistant to environmental stress

XX Gamma -tocopherol methyltransferase; gamma-TMT; SLR0089; 165H5T7; meat;
 KW transgenic plant; alpha-tocopherol; gamma-tocopherol; forage plant.
 XX
 OS *Synechocystis* sp.
 XX WO9504622-A1.
 PN XX DE SpnL protein involved in spinosyn biosynthesis.
 XX PD Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal
 XX KW microclides; arachnid; nematode; insect; polyketide; polyketide synthase;
 PF 22-JUL-1998; 98WO-US15137.
 XX PKS; extender module; initiator module; acyl transferase domain; AT;
 PR 17-JUL-1998; 98US-0053819.
 PR 25-JUL-1997; 97US-005819.
 PR 26-JAN-1998; 98US-0072497.
 XX
 PA (UYNE-) UNIV NEVADA.
 XX PI Dellapenna D, Shintani DK;
 XX DR WPI; 1998-142458/12.
 DR N-PSDB; AAX17788.
 XX PT Newly isolated DNA fragment comprising a γ -tocopherol (vitamin E) methyltransferase coding sequence - useful for producing γ -tocopherol, and transgenic plants, seeds and oils with an altered tocopherol profile
 PS XX
 XX PI Example 2; Page 33-35; 46pp; English.
 CC The invention provides DNA sequences encoding gamma-tocopherol methyltransferases (gamma-TMT). The gamma-TMT encoding genes SLR0089 and 165H5T7 are isolated from *Synechocystis* and *Arabidopsis* species respectively. The DNA fragments are useful for producing transgenic plants containing a higher alpha-tocopherol:gamma-tocopherol ratio. They are also useful for producing alpha-tocopherol and plants with increased gamma-tocopherol, which may be useful in certain industries such as the meat industry e.g. for developing forage plants to feed animals. The production of transgenic plants (and seeds) with a higher alpha-tocopherol:gamma-tocopherol ratio, using the gamma-TMTs, will increase the level of alpha-tocopherol in the human diet, in addition to enhancing the stability and shelf life of plants and plant products. Increased levels of alpha-tocopherol will also increase meat quality and extend shelf life of post-processed meat products. Plants with a higher alpha-tocopherol:gamma-tocopherol ratio may also produce advantageous phenotypes. The present sequence represents a *Synechocystis* gamma-TMT.
 XX SQ Sequence 317 AA;

Query Match 7.9%; Score 204.5; DB 20; Length 317;
 Best Local Similarity 26.3%; Pred. No. 8.2e-11; Mismatches 61; Conservative 48; Mismatches 90; Indels 33; Gaps 8;
 OY 215 YVKRKKNQIQISWVQKVSDEDRKGQFRFLDSSQYKFNSTRYRVEFGPGYVSTGGLET 274
 Db 35 yekknfyddsglwedvrg-----lmmhgyyqphgtyrid-----raqidil 80
 OY 275 KEF----YSKLDLPGOKYLVGGGGDFYMFAMYDVVVGDLSTINMISFALE--RS 328
 Db 81 kelawaqpqnsalkp-rkldlgqgggsslyaaqhaeavmgaslpvqveragerara 139
 OY 329 IGLKCAVEEVADOTKKDOPENSDVVISRTDTHIQDKPALFRSFHKULKPGCKVLSD 388
 Db 140 lqg9stcgvqanadlpfasdsfdwwslesgahmpnkqfqleawrvlpkgplilat 199
 OY 389 YC----KSAGTPAEEFAVYRQDHL----DVKAYGKMKDAGGEV 429
 Db 200 wchxpidpangpltderrhl-qaiydyvclpyvsvlpdyeaiaearecgfgei 250

Sequence 283 AA;

Query Match 7.6%; Score 198; DB 20; Length 283;
 Best Local Similarity 25.7%; Pred. No. 2.8e-10; Mismatches 53; Conservative 44; Mismatches 97; Indels 12; Gaps 5;

RESULT 4 AAY39308

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PR	18-JUN-1999; 990US-0139763.	PR	27-AUG-1999; 990US-0151066.
PR	22-JUN-1999; 990US-0139817.	PR	27-AUG-1999; 990US-0151080.
PR	23-JUN-1999; 990US-0139899.	PR	30-AUG-1999; 990US-01511303.
PR	23-JUN-1999; 990US-0140353.	PR	31-AUG-1999; 990US-01511438.
PR	01-JUL-1999; 990US-0140354.	PR	01-SEP-1999; 990US-01511930.
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PR	08-JUL-1999; 990US-0142803.	PR	13-SEP-1999; 990US-0153758.
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Best Local Similarity 27.3%; Pred. No. 2.6e-09; Matches 65; Conservative 36; Mismatches 93; Indels 44; Gaps 7;

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Db	149	vkadfmkmpfpensfdavvayiaeachapdaygycekeiyrvlpkqcfayewcmtdarfp 208
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QY	209	dnaehqkikgeleigdglpdirlttkcileaklgqaf-eviweklakdsspvpwylpldkn 267

QY	397	SAEFAYIR--ORGDLHDKWAKG--MKDAGNEVIAENR-----	434
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QY	435	-----TDQFQVQLOKELDALEOEKKDFIDPSEEDYNDLVDGWKAEL	476
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DT	17-OCT-2000 (first entry)		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 24111.		
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KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.		
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OS	Arabidopsis thaliana.		
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Query Match

7.2%; Score 188; DB 21; Length 366;

Best local similarity	27.3%	Pred.	No.	3-6s-09;	Matches	65;	Conservative	36;	Mismatches	93;	Indels	44;	Gaps	7;
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PR	22-JUL-1999;	9905-0145086.	PR	18-OCT-1999;	9905-0159584.
PR	21-JUL-1999;	9905-0145145.	PR	21-OCT-1999;	9905-0160741.
PR	23-JUL-1999;	9905-0145218.	PR	21-OCT-1999;	9905-0160767.
PR	23-JUL-1999;	9905-0145224.	PR	21-OCT-1999;	9905-0160768.
PR	26-JUL-1999;	9905-0145276.	PR	21-OCT-1999;	9905-0160770.
PR	27-JUL-1999;	9905-0145913.	PR	21-OCT-1999;	9905-0160815.

PR 25-OCT-1999; 99US-0161405.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 29-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 7.2%; Score 187; DB 21; Length 293;
 Best Local Similarity 27.3%; Pred. No. 3.2e-09; Gaps
 Matches 65; Conservative 36; Mismatches 93; Indels 44; Gaps 7;

Qy 280 KLDLKGOKVLVDVGCGGGDFYMAENYDNEVVGIDUSINMTSFA--LERSIGLKCAVEF 337
 Db 46 qgqgqpgqkvldvgcgqgqplreiarisnsvvtglnnoneyqitrgkeinrlagdkcnf 105
 Qy 338 EVAADCTKKDYPENSFDVITYSRDMLHTQDKPALFRSEHKWLKPGKVLLSDYCKS-AGTP 396
 Db 106 vkadfmkmpfensfdavyaiteatcphdaycyekeyrvkpgqcfayewomtdafp 165
 Qy 397 SAEFAAVIR--QRGYDLDHYRAYK--MLKDAGFTEVIAHR----- 434
 Db 166 diaehqklikgeleigdldpdirtkclealkqagf-eviwekdlakdsspvpwypldkn 224
 Qy 435 -----TDOFIQVILQKELDALEQEDPFDSEEDNDIVDGWAKL 476
 Db 225 hfsllssfrtavgrfitknvkill--eyirlapqgsqrvsnfileqaeglvdggrre 280

Search completed: September 20, 2001, 16:18:12
 Job time: 225 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: September 20, 2001, 16:16:42 ; Search time 13.12 Seconds
(without alignments)
775.277 Million cell updates/sec

Title: US-09-525-885-2
Perfect score: 2598
Sequence: 1 MRASAMGVILQREVFKKWI.....KLVRTPEGEQWNLFIKKM 494
scoring table: BIOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	8.0	363	4	US-09-041-718-5
2	198	7.6	283	4	US-09-036-987A-13
3	179	6.9	280	4	US-09-039-603-2
4	172.5	6.6	282	1	US-08-457-245-9
5	170	6.5	383	4	US-09-041-718-3
6	168	6.5	275	4	US-09-036-987A-7
7	160	6.2	361	4	US-09-041-718-4
8	148.5	5.7	376	4	US-09-041-718-2
9	128.5	4.9	276	3	US-08-935-263-16
10	128.5	4.9	308	1	US-08-457-245-8
11	122.5	6	5346025	8	Patent No. 5386025
12	120	4.6	1084	1	US-08-455-543A-56
13	120	4.6	1084	2	US-08-223-305C-56
14	120	4.6	1103	1	US-08-455-543A-53
15	120	4.6	1103	2	US-08-223-305C-53
16	115	4.4	287	1	US-08-457-245-3
17	114.5	4.4	1091	1	US-07-745-206A-25
18	114.5	4.4	1091	2	US-08-455-543A-52
19	114.5	4.4	1091	3	US-08-311-363-25
20	114.5	4.4	1091	3	US-08-713-118-4
21	114.5	4.4	1091	3	US-08-457-207-4
22	114.5	4.4	1091	4	US-09-452-007-4
23	114	4.4	1079	1	US-08-455-543A-55
24	114	4.4	1079	2	US-08-223-305C-55
25	113.5	4.4	1106	1	US-08-425-675B-5
26	110.5	4.3	1106	1	US-08-336-257A-8
27	108.5	4.2	1086	1	US-08-452-543A-54

RESULT 1
US-09-041-718-5
Sequence 5, Application US/09041718A
Patent No. 6225075

GENERAL INFORMATION:
APPLICANT: Bard, Martin
TITLE OF INVENTION: DNA encoding sterol methyltransferase
FILE REFERENCE: 740.003US1
CURRENT APPLICATION NUMBER: US/09/041-718A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 5
LENGTH: 363

TYPE: PRT
ORGANISM: Triticum aestivum
US-09-041-718-5

ALIGNMENTS

Query Match 8.0%; Score 207; DB 4; Length 363;
Best Local Similarity 28.6%; Pred. No. 3.9e-12; Mismatches 88; Indels 44; Gaps 8;

Matches 68; Conservatism 38; Description

QY 280 KLDIKPGKVLDVGIGGIGGDYMANYYDVEVGIDLISNMS-FALERSIGLICAVEF 337
Db 114 QLEIKPGMKVLDVGIGGIGGLREIRFSSSTVGTGNNNDYQITRKALNSVGLATCDF 173

QY 338 EVADCTKKDYPENSFDWVYRSRDTILHIDQKPAFLRSFSFKHNLKPGKVLISDYC-KSAGTP 396
Db 174 VKADFMKMPFSDNTFDDAVYALETACHADPVGCGYKIRVYLPGOCFAVYEWCIIDHYD 233

QY 397 SAEFFAYIR--QRYDLHDYKAYKML--KDAGFVEV-----AENR----- 434
Db 234 NNATHKRIKOLEIELGNGLDIRLIRSTQCLQAVKDAEEDSWDWDKAEDSLPWPYILPDS 292

QY 435 -----TDOPTQVLOKEDALEQKDFFDIDFSESDYNDIVGWAKL 476
Db 293 RFSLSLSFRLLTVGRITRNNAVKL--EYVGIAPESSQRVSFLEXAAGLVEGGKEI 348

RESULT 2
US-09-036-987A-13
Sequence 13, Application US/09036987A
Patent No. 6143526

GENERAL INFORMATION:
APPLICANT: Balt, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.

APPLICANT: Treadaway, Patti J. ; EARLIER APPLICATION NUMBER: PCT/EP96/03643
 APPLICANT: Turner, Jan R. ; EARLIER FILING DATE: 1996-08-19
 APPLICANT: Waldron, Clive
 TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
 TITLE OF INVENTION: Production
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dow AgroSciences LLC Patent Department
 STREET: 9330 Zionsville Road
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: USA
 ZIP: 46268
 COMPUTER READABLE FORM:
 COMPUTER TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/036, 987A
 FILING DATE: 09-MAR-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Stuart, Donald R
 REGISTRATION NUMBER: 28,479
 REFERENCE/DOCKET NUMBER: 50,608
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317)337-4816
 TELEFAX: (317)337-4847
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 283 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ;
 ; US-09-036-987A-13

Query Match 7.6%; Score 198; DB 4; Length 283;
 Best Local Similarity 25.7%; Pred. No. 2e-11; Mismatches 5;
 Matches 53; Conservative 44; Mismatches 97; Indels 12; Gaps 5;
 QY 272 ETTKERYPSKDLQPKGOKVYLDVGCGIGGGDFYMAENYDVVEVGGIDLSINMISFA--LERSIGLKAVEEFADCTKKOYPENSF 294
 Db 38 QLTDLFIDKAALRPGAHLFDLGCGNGOPVVRACASGVRVIGITVHQAHLAATRPLANET 97
 Qy 330 GUJKCAYEEFADCTKKOYPENSFDVYIYSDTILHTQDKPALERSPKHKLKGKGKVLSIDY 389
 Db 98 GLAGSLFEDLVQAGQLPYDPGFQAAWAMQSVQVOTVDOAAIREVHRLPEPGGRFLVLDI 157
 Qy 390 CKSAGIPSAEFAAYIRGQYDHLVDAKYGKMLKDAGF---VEVIAENR-TDQFQVL 442
 Db 158 ITRVRILPE-EPAAV-WTGTAHTLNSFTALVSEAFREILEVTDLIAQTCRWMSWVDEL 214
 Qy 443 QKELDALEQKDFIDFSEEDYNDI 468
 Db 215 LRKLDDELAGVERAAGTYQQYRVLGDI 240
 ;
 RESULT 4 US-09-457-245-9
 ; Sequence 9, Application US/09457245
 ; Patent No. 5573915
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: BARRY III, Clifton E.
 ;
 ; APPLICANT: XUAN, Ying
 ;
 ; TITLE OF INVENTION: THE BIOSYNTHESIS OF CYCLOCOPROPANTED MYCOLIC ACIDS IN
 ; NUMBER OF SEQUENCES: 21
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: Steuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ;
 ; COMPUTER READABLE FORM:
 ;
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US/09/457, 245
 ;
 ; FILING DATE:
 ;
 ; CLASSIFICATION: 435
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ;
 ; NAME: Chambers, Guy W.
 ;
 ; REGISTRATION NUMBER: 30,617
 ;
 ; REFERENCE/DOCKET NUMBER: 15280-216000
 ;
 ; TELECOMMUNICATION INFORMATION:
 ;
 ; TELEPHONE: (415) 543-9600
 ;
 ; TELEFAX: (415) 543-5043
 ;
 ; INFORMATION FOR SEQ ID NO: 9:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ;
 ; LENGTH: 282 amino acids
 ;
 ; TYPE: amino acid
 ;
 ; STRANDEDNESS: not relevant

APPLICANT: Bard, Martin
 TITLE OF INVENTION: DNA encoding sterol methyltransferase
 FILE REFERENCE: 740 03051
 CURRENT APPLICATION NUMBER: US/09/041,718A
 CURRENT FILING DATE: 1998-03-13
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 361
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-09-041-718-4

RESULT 8
 Query Match 6.2%; Score 160; DB 4; Length 361;
 Best Local Similarity 23.6%; Pred. No. 1.6e-07;
 Matches 59; Conservative 41; Mismatches 110; Indels 40; Gaps 9;
 Qy 213 GAVVSKKKNQNOISWLW-----QKVDSEDDKGQRFQFLDSQQYKFNSILRVER 260
 Db 39 GGSISAAKVKQDNYKQYNSFRPKEIETAAKQVWQVLDVGGIGGGDFYAAENYDVEVWQIDL 316
 Qy 261 FGGYVSTGGLETTK---EFVSKDLIKPGQVWLDVGGIGGGDFYAAENYDVEVWQIDL 316
 Db 95 FSPSIPCKSHKAATRUEMAYDILQIQKPGQKILDVCGVGPPMRAASHSRANVYGITI 154
 Qy 317 SNNMISPAF--EBSIGIKCAVREPEVADCTKKDYPENSFDVTSRDTTIIHQPKALFRSF 374
 Db 155 NEYQVNKRHLHKKAGLDALCEVVCVGNFLQMPFDNSFDGAYSIEATCHAPLEVAEI 214
 Qy 375 HWKLPKGKVLSYDCKSAGTSAEFA---YIR----ORGYDLDVKA---GMLK 422
 Db 215 YRVLKPG----SMVSYEWVTEKFKAEDDEHVEVIOGIERGALPGLRAYVDIAETAK 269

Qy 423 DAGFVETVIA 432
 Db 270 KVGF-EIVKE 278

RESULT 9
 Query Match 6.2%; Score 16; DB 16;
 Best Local Similarity 22.9%; Pred. No. 0.00013;
 Matches 65; Conservative 45; Mismatches 97; Indels 77; Gaps 13;
 Qy 11 ERREVFKKWIERSVUDLVEAMMLDSOASDILKVERPEVLHMLPPYEGK--SVLELAGI 67
 Db 3 DQQLLSKRKFSEH-----AKTYDATA-NVKQNMAKOLVLDLJPOKSKQRNINLEGGT 54
 ; GENERAL INFORMATION:
 ; PATENT NO. 6225075
 ; PATENT: Bard, Martin
 ; TITLE OF INVENTION: DNA encoding sterol methyltransferase
 ; FILE REFERENCE: 740 03051
 ; CURRENT APPLICATION NUMBER: US/09/041,718A
 ; CURRENT FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 376
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-041-718-2

Query Match 4.9%; Score 128.5; DB 3; Length 276;
 Best Local Similarity 22.9%; Pred. No. 0.00013;
 Matches 65; Conservative 45; Mismatches 97; Indels 77; Gaps 13;
 Qy 11 ERREVFKKWIERSVUDLVEAMMLDSOASDILKVERPEVLHMLPPYEGK--SVLELAGI 67
 Db 3 DQQLLSKRKFSEH-----AKTYDATA-NVKQNMAKOLVLDLJPOKSKQRNINLEGGT 54
 Qy 68 GRFTGELAE--KASQVIAFLFIESVTKKNESINGHYKVNPKMCADYTPSPNISPNVDI 125
 Db 55 GYLTLRLVNTFPNASITAVDIAJAPGMVVAKGITME-DRVTRLCADIEEMTLN--ENYDL 110
 Qy 126 IFSNWLLMLSDPEEVERLVERMLWKLWKLPGGIFFRFESCFHOSGDHRRKSNTPHYRPFY 185
 Db 111 IISNATFOWLN--LQCTIQLFTRJTPEGULIF-----STEG 146
 Qy 186 TKTIFKECHMQDGSNSYELSLTGCKCIGAYYRSKKMNQISWLWQVDSEDDKGFRFLD 245
 Db 147 IKTFQELHM-----SVE-----HAKER-----LQLSIDSSQQLYALEE 181
 Qy 246 SSOYKNSILRYERVFGPGYVSTGGLETTKHFVSKLDLKPQKV 289
 Db 182 LSQICEERAI-----PFSSAAPPLEITK--IEKLELEYFQTV 214

RESULT 10
 Query Match 5.7%; Score 148.5; DB 4; Length 376;
 Best Local Similarity 24.0%; Pred. No. 2.3e-06;
 Matches 63; Conservative 42; Mismatches 102; Indels 55; Gaps 12;
 Qy 229 WOKVSDDDKGQYQRFQFLSSQ-----YKENSILRYERVFGPGYVSTGGLETT 274
 Db 53 WDGGSISKDEE-KRLNDYPSOLTHHYYNLVTDFYEEWGNSSFHFSRY-KGERAFRQATH 110
 Qy 275 KFLDKPGQKVLDVGGIGGGDFYMAENYDVERVGLDLSIINMISPLERS--- 328
 Db 111 EHFLAKMNLNENMVKVLDVGCGVGGPQREIRPFTDCEIVG---LNNNDYQIERNHYAK 166
 Qy 329 -IGLKGCAVEFEVADCTPKDYPENSDVYIYSRQITLHQDKPALKFSPHKWLPKGKVLIS 387
 Db 167 KIHLHKLSYVKGFMQMDPEPESTDAVIAERAVHAPLEGVSETYKVLRPG---- 221

RESULT 9
 Query Match 6.2%; Score 16; Application US/08935263A
 Sequence 16, Application US/08935263A
 Patent No. 6117669
 ; GENERAL INFORMATION:
 ; APPLICANT: Furuchi, Yasuhiro
 ; APPLICANT: Hosino, Tatsuo
 ; APPLICANT: Kimura, Hitoshi
 ; APPLICANT: Kiyasu, Tatsuya
 ; APPLICANT: Nadahashi, Yoshie
 ; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 ; FILE REFERENCE: Biotin Genes
 ; CURRENT APPLICATION NUMBER: US/08/935, 263A
 ; CURRENT FILING DATE: 1997-09-22
 ; EARLIER FILING DATE: 1996-09-27
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 276
 ; TYPE: PRT
 ; ORGANISM: Kurthia sp.
 US-08-935-263-16

RESULT 8
 Query Match 6.2%; Score 16; Application US/08935263A
 Sequence 16, Application US/08935263A
 Patent No. 6117669
 ; GENERAL INFORMATION:
 ; APPLICANT: Furuchi, Yasuhiro
 ; APPLICANT: Hosino, Tatsuo
 ; APPLICANT: Kimura, Hitoshi
 ; APPLICANT: Kiyasu, Tatsuya
 ; APPLICANT: Nadahashi, Yoshie
 ; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 ; FILE REFERENCE: Biotin Genes
 ; CURRENT APPLICATION NUMBER: US/08/935, 263A
 ; CURRENT FILING DATE: 1997-09-22
 ; EARLIER FILING DATE: 1996-09-27
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 276
 ; TYPE: PRT
 ; ORGANISM: Kurthia sp.
 US-08-935-263-16

RESULT 8
 Query Match 6.2%; Score 16; Application US/08935263A
 Sequence 8, Application US/08935263A
 Patent No. 6117669
 ; GENERAL INFORMATION:
 ; APPLICANT: BARRY III, Clifton E.
 ; APPLICANT: YUAN, Ying
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA INVOLVED
 ; TITLE OF INVENTION: IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOLIC ACIDS IN
 ; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khouri and Crew

STREET: Stewart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/457.245
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Chambers, Guy W.
 REGISTRATION NUMBER: 30,617
 REFERENCE/DOCKET NUMBER: 15280-216000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 308 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Mycobacterium leprae
 US-08-457-245-8

Query Match 4.9%; Score 128.5; DB 1; Length 308;
 Best Local Similarity 22.5%; Pred. No. 0.00016; Mismatches 56; Conservatve 32; Indels 73; Gaps 9;

Qy 278 VSKDLKPGQKVLDVGCGGGDDYMAENYDVEVGIDLSINMSFALSERSIGLKCAVEF 337
 Db 68 LSKIGLGERGMLLIDIGCGWGSTMLHAIEKDVNTIGLTSANOLAHN-----KLF 118

Qy 338 EVADCTKKDYP-----EINSDFVYISRDTLHQD-----KPALFRSEHKKW 377

Db 119 AEIHDHTRTDKDVRQLOGWEQFDPVDRITSLGAREFHADGAGDPERYDSFHKMCYD 178

Qy 378 LKPGKVLI-----SDYCKSAG---TBSA---EPAAYTQRGYQYLDVYKAYGKMLK--- 422

Db 179 LPDDGMLRHTITVDPDAKETKELGTTTPMSLRLKFT-----LTETPGGRPKISQV 232

Qy 423 -----DAGFVEVIAENRTDFOIQVQLQKELDALEQKDDF----- DD 459

Db 233 DHYSSNAGTVERHRIGSHYVPTINAWAALEAHKDEIALQCRQIVDYMHLTGCD 292

Qy 460 FSEEDYNDI 468

Db 293 LFRRTYTDV 301

RESULT 11
 5386025-8

PATENT NO. 5386025
 APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL
 M.; CAMPBELL, KEVIN P.
 TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 9
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/482,384

APPLICATION NUMBER: US/07/482,384

FILEING DATE: 20-FEB-1990

SEQ ID NO:8
 LENGTH: 1086
 5386025-8

Query Match 4.7%; Score 122.5; DB 6; Length 1086;
 Best Local Similarity 20.3%; Pred. No. 0.0043; Mismatches 96; Conservatve 66; Indels 155; Gaps 25;
 Matches 96; Conservatve 66; Mismatches 156; Indels 155; Gaps 25;
 Qy 77 KASQVIALDFIESVIK-----KNESTINGHYKVNKFMCADYTSPLNISPNVDIIFSN 129
 Db 554 KSQRPVTLDFDAELNDIKVETRNKMDGEGESEKTFRL-YKSQDRYIDGNRNTVLT 612
 Qy 130 WLLMVLSDBEVERIVE-RMKWIKP-----GGYIFF--RESC-----FHO 166
 Db 613 YSFVYIKAKIEETTOARYSETLKPDNFEESGYTLAPRDYCSLDKFSNDNTTEFLNFE 672
 Qy 167 SGDIKRKSNPHTYREPFYTKFKECHMODSCNSYNSYELSLIGCKCIGAVSKRN----- 221
 Db 673 FIDRKTPNNPS-----CNDLTLNRYLL-----VQYWSKQKNIGVK 717
 Qy 222 -----QNQIISWLWQK-VSEDDKGQFRELDSSQYKFNSLRVRVFGCYV 266
 Db 776 ESGIMVKAVELVIQGKLIKPA-----WVGKIDVNNENF 811
 Qy 325 LERSGIKCAVEFADCKDYPENSERDVYISRDTLHQD-----KPALFRSEHKKW 375
 Db 812 TKTSIRDPCA---GVCDCKR---NS-DVM---DCVI-----LDDGFL 844
 Qy 385 LIS---DICKSAG-----TPS-----REFAAVIRQRYDHLVYKAGKMLK-----AG 425
 Db 845 LMANHDDYTNQIGRFGEIDPSLMRHLVNSIVYAFNSYDYSOVCCEPGAAPKOGAGHRSA 904
 Qy 426 FVEVIAE-----NRTQDFIQVLT-OKELDALEQKDDFIDDFSEE 463
 Db 905 YVPSIADIQIIGWATAAAWISIQLQFLLSPRLEADMEDDFTASMSKQ 957

RESULT 12
 US-08-455-543A-56
 Sequence 56, Application US/08455543A
 Patent No. 5792846
 GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILEING DATE: May 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILEING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILEING DATE: April 10, 1992
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206 ; Sequence 56, Application US/08223305C
 FILING DATE: 15-AUG-1991 ; Patent No. 585824
 PRIOR APPLICATION DATA: ; GENERAL INFORMATION:
 APPLICATION NUMBER: US 07/620,250 ; APPLICANT: Harpold, Michael
 FILING DATE: 30-NOV-1990 ; APPLICANT: Ellis, Steven
 PRIOR APPLICATION DATA: ; APPLICANT: Williams, Mark
 APPLICATION NUMBER: US 07/603,751 ; APPLICANT: Feldman, Daniel
 FILING DATE: 04-APR-1989 ; APPLICANT: McCue, Ann
 PRIOR APPLICATION DATA: ; APPLICANT: Brenner, Robert
 APPLICATION NUMBER: WO PCT/US89/01408 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 FILING DATE: 04-APR-1989 ; NUMBER OF SEQUENCES: 57
 PRIOR APPLICATION DATA: ; CORRESPONDENCE ADDRESS:
 APPLICATION NUMBER: US 07/176,899 ; ADDRESSEE: Brown, Martin, Haller & McClain
 FILING DATE: 04-APR-1988 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 NAME: Seidman, Stephanie L. ; COUNTRY: USA
 REGISTRATION NUMBER: 33,779 ; ZIP: 92101-926
 REFERENCE/DOCKET NUMBER: 6362-52517 ; COMPUTER READABLE FORM:
 TELECOMMUNICATION INFORMATION: ; MEDIUM TYPE: Diskette
 TELEPHONE: (619)238-0999 ; COMPUTER: IBM Compatible
 TELEFAX: (619)238-0062 ; OPERATING SYSTEM: DOS
 INFORMATION FOR SEQ ID NO: 56: ; SOFTWARE: FastSEQ Version 1.5
 SEQUENCE CHARACTERISTICS: ; CURRENT APPLICATION DATA:
 LENGTH: 1084 amino acids ; APPLICATION NUMBER: US/08/223,305C
 TYPE: amino acid ; FILING DATE: April 4, 1994
 STRANDEDNESS: single ; PRIOR APPLICATION DATA:
 TOPOLOGY: linear ; APPLICATION NUMBER: 07/868,354
 MOLECULE TYPE: protein ; FILING DATE: April 10, 1992
 FRAGMENT TYPE: internal ; PRIOR APPLICATION DATA:
 US-08-455-543A-56 ; APPLICATION NUMBER: US 07/745,206
 ; PRIOR APPLICATION DATA:
 ; FILING DATE: 15-AUG-1991
 ; APPLICATION NUMBER: US 07/620,250
 ; PRIOR APPLICATION DATA: ; FILING DATE: 30-NOV-1990
 ; APPLICATION NUMBER: WO PCT/US89/01408 ; PRIOR APPLICATION DATA:
 ; FILING DATE: 20-FEB-1990 ; APPLICATION NUMBER: US 07/482,384
 ; PRIOR APPLICATION DATA: ; FILING DATE: 04-APR-1989
 ; APPLICATION NUMBER: US 07/603,751 ; PRIOR APPLICATION DATA:
 ; FILING DATE: 04-APR-1989 ; APPLICATION NUMBER: US 07/176,899
 ; PRIOR APPLICATION DATA: ; FILING DATE: 04-APR-1988
 ; APPLICANT/AGENT INFORMATION: ; NAME: Seidman, Stephanie L.
 ; APPLICANT/AGENT INFORMATION: ; REGISTRATION NUMBER: 33,779
 ; APPLICANT/AGENT INFORMATION: ; REFERENCE/DOCKET NUMBER: 52516 (P519739)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619)238-0999 ; INFORMATION FOR SEQ ID NO: 56:
 ; TELEFAX: (619)238-0062 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1084 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-223-305C-56
 ;
 Query Match 4.6% ; Score 120; DB 1; Length 1084;
 Best Local Similarity 19.6%; Pred. No. 0.0075%; Gaps 26;
 Matches 94; Conservative 76; Mismatches 158; Indels 152; Gaps 26;
 ;
 QY 77 KASQVIALDFIESVIK-----KNESTINGHKNVKFMC-----ADWTS 115
 Db 533 KSQEPVILDFDLEELNDIKVIRNKWIDGESGEKTRTLVKSQDERYIDKCNRRVWTP 592
 Qy 116 LNISPNSVUDIIFSNWMLMLYSLSDVEEVLVE-RMLKWLKP-----GGYIFF--RESC--- 163
 Db 593 VNGTDYSLALVLPITYKAKLEETITQARYSETLKDQNFEESGYTFIAPRDYCNDL 652
 Qy 164 -----PHQSGHHRKRNPNTHPREPYRTKIKECHQHDSDNSY --ELSLIGC 209
 Db 653 ISDNNTTEFLLNPNFIDRKTPNNSCNRD--LINVRLDAGFTNELVONYWSQKNIKGV 710
 Qy 210 KC-----IGAVVKSKKNQIQISWLWQK-VDSEDDKGQFLDSSQYKFNSILRVERV 260
 Db 711 KARFWVWDGGITRVYPREAGEN----WQENNETYEDSFYKRSLNDNYVFTA--PYFNK 763
 Qy 261 FSPGYYVSTGGL--ETKEFVKSLKDLKPGQVKLDVGCGIGGDFYMAENYDVWVGDLSI 318
 Db 764 SGPGAYESGIMVSKAVEYIYQKLKPA-----VVGKIDV 799
 Qy 319 N-MISFALERSTGCKCAFEVADCKKDPYNSFDIYVSRDTILHQLDKPALFRSHK 377
 Db 800 NSWIENFTKTSIRDPCKA--GPVCDCKR--NS-DVM---DCVY----- 833
 Qy 378 LKPGYKVLIS---DYCKSAG----TPS-----AEFAAYRQRGYDLDHYKAYGMLKD 423
 Db 834 LDDGGFLMLMHDDYTNQIGRFFGEIDPSLMLHVLNIVSYAFNKSVDYQSYCEPAGPK 893
 Qy 424 -----AGFVETIAE-----NRTDQFIOVI--QKELDAFOEKDDFDFSEE 463
 Db 894 GAGHRSAYVPSVADLQIGWWATAAANSILOOFLSLFPRULEAVEMDDDFTASLSQ 953
 ;
 Query Match 4.6% ; Score 120; DB 2; Length 1084;
 Best Local Similarity 19.6%; Pred. No. 0.0075%; Gaps 26;
 Matches 94; Conservative 76; Mismatches 158; Indels 152; Gaps 26;
 ;
 Qy 77 KASQVIALDFIESVIK-----KNESTINGHKNVKFMC-----ADWTS 115
 ;

APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 PRIORITY APPLICATION DATA:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE DOCKET NUMBER: 6392-52517
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1103 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 ; US-08-455-543A-53
 ; US-08-455-543A-53
 ; Sequence 53, Application US/08455543A
 ; Patent No. 5,792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2936
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIORITY APPLICATION DATA:
 ; RESULT 14
 ; US-08-455-543A-53
 ; Sequence 53, Application US/08455543A
 ; Patent No. 5,792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2936
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIORITY APPLICATION DATA:
 ; RESULT 15
 ; US-08-223,305C-53
 ; Sequence 53, Application US/08223305C
 ; Patent No. 5,51824
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven

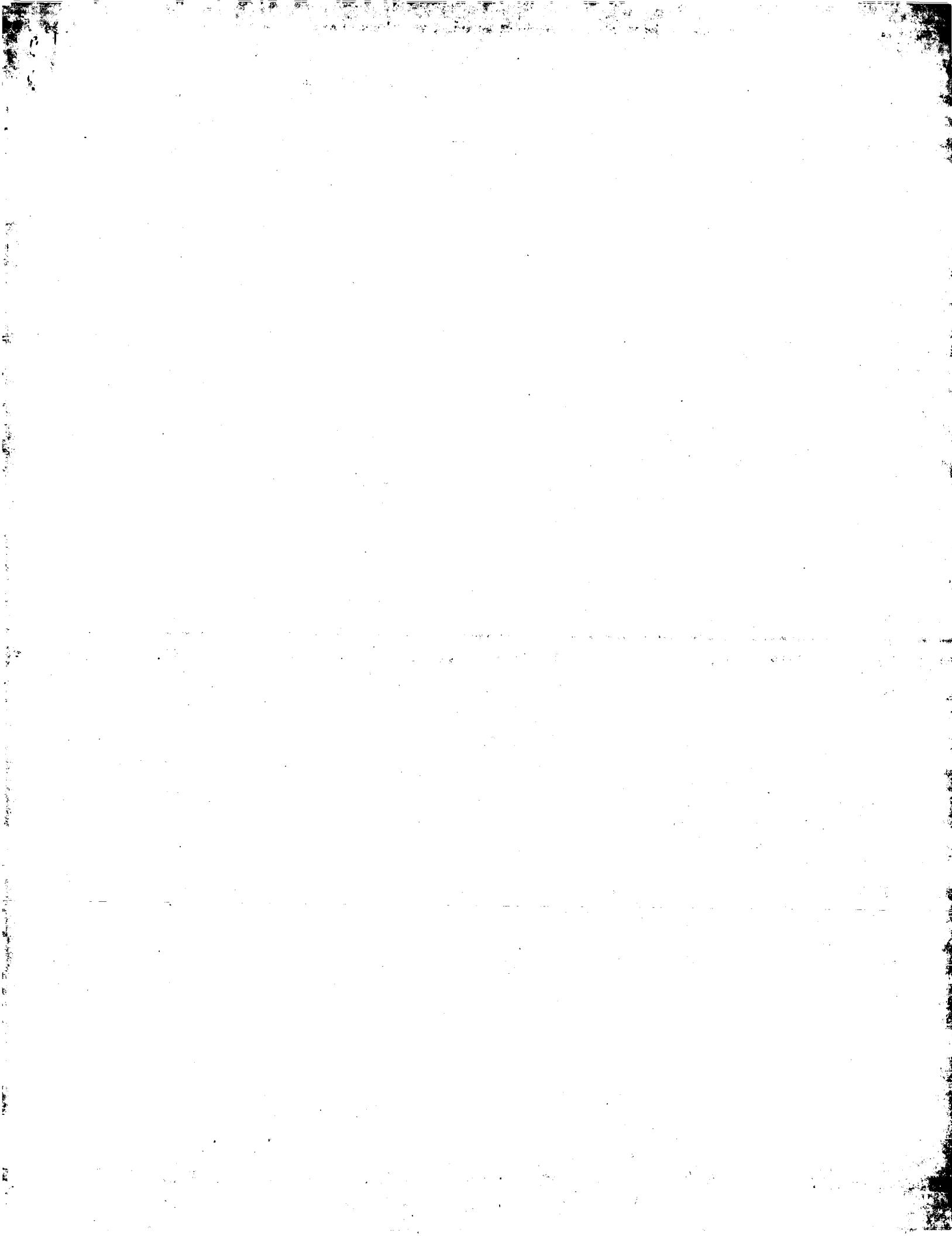
Search completed: September 20, 2001, 16:19:43
Job time: 181 sec

Best Local Similarity	19.6%	Score: 120.0	DB: 2	Length: 1103
Matches	94	Conservative	76	Mismatches 158; Indels 152; Gaps 26;

Y 77 KASOVIALDFIESVIK -----KNEISINGHYKVNKFMC -----ADVTSPS 115
b 552 KSOEPVMTDAELDIKTEIRNMKGDEGEKFTPLVKSDERVTDKGNTYTWP 611

Thu Sep 20 16:26:00 2001

us-09-525-885-2.rai



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2001, 16:17:22 ; Search time 17.12 Seconds
(without alignments)
2198.027 Million cell updates/sec

Perfect score: US-09-525-885-2
Sequence: 1 MAASANGVLOBREVFKYWI..... KLVRTTEGEQQWGLFIKKM 494.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:68:*

1: PIRI:*

2: pIRI:*

3: pIRI:*

4: pIRI:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	2086	80.3	555	hypothetical protein H96762
2	1287.5	49.6	374	protein TIN15_23 [hypothetical protein]
3	498.5	19.2	437	hypothetical protein
4	449.5	17.3	495	hypothetical protein
5	207	8.0	363	probable 24-sterol hypothetical protein
6	204.5	7.9	317	probable 24-sterol cyclop propane fatty
7	191	7.4	367	hypothetical protein
8	189.5	7.3	387	hypothetical protein
9	187.5	7.2	227	probable 24-sterol cyclop propane fatty
10	185	7.1	318	probable cyclopropyl 24-sterol C-methyl
11	183.5	7.1	462	probable cyclopropyl 24-sterol C-methyl
12	182	7.0	344	probable cyclopropyl 24-sterol C-methyl
13	182	7.0	344	probable cyclopropyl 24-sterol C-methyl
14	177	6.8	348	gamma tocopherol m
15	176.5	6.8	306	tryG protein - Sac
16	176	6.8	382	cyclop propane fatty
17	176	6.8	382	cyclopropane fatty
18	175.5	6.8	283	probable cyclopropane fatty
19	174.5	6.8	227	probable cyclopropane fatty
20	173	6.7	346	probable cyclopropane fatty
21	171	6.6	389	probable cyclopropane fatty
22	170.5	6.6	283	probable cyclopropane fatty
23	170	6.5	383	probable cyclopropane fatty
24	166	6.4	389	probable cyclopropane fatty
25	165.5	6.4	366	probable cyclopropane fatty
26	163.5	6.3	254	probable cyclopropane fatty
27	162.5	6.3	581	probable cyclopropane fatty
28	161.5	6.2	378	probable cyclopropane fatty
29	160	6.2	361	probable cyclopropane fatty

RESULTS

RESULT	1
H96762	hypothetical protein F6D5_1 [imported] - Arabidopsis thaliana
C-Species: Arabidopsis thaliana (mouse-ear cress)	C-Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C-Accession: H96762	R-Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A.; Autors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Autors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Taloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A-Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.	A-Reference number: A86141; MUID:21016719
A-Accession: H96762	A-Status: preliminary
A-Molecule type: DNA	A-Residues: 1-555 <STO>
A-Cross-references: GB:AE005173; NID:gi10092368; PIDN:AGI12776_1; GSPDB:GN00141	A-Genetics: C;Gene: F6D5_1
A-Map position: 1	Query Match 80.3%; Score 2086; DB 2; Length 555; Best Local Similarity 77.7%; Pred. No. 7.1e-139; Mismatches 42; Indels 0; Gaps 0; Qy 10 QEREVFKYWIENSYDLTVEAMMDSQASDQLKVERPEVLSMLPPYEGSVLELGAGTCR 69 Db 71 EERBQKWNKWEVNLKQVLSMAMMDSKLDKREPERLAFPLPIEGTVLRLGAGCR 130
Qy	70 FTGELBLAKQSQVFLDFIESVIKKNESTINGHYKWKFMCAWDVTFPSLNTPNSVDFIFSN 129
Db	131 FTTELAQKAGQVIAWDFTESVKRNNTNGHYKWKFLADVPSNMPNEPSMDFLFSN 190
Qy	130 WLMLYLSDBEVEVERVERMLKWLKPGGYAFFRESCFHQSQDIIKRSKSNPHTYREPREYTKIF 189
Db	191 WLLMLYLSDOEVEDLAKKMLQWTKVGGYAFFRESCFHQSQDIIKRSKSNPHTYREPREYTKIF 250
Qy	190 KECHMDQDSGSNSYELSLIGCKCCTGAYVSKKNQNLISWIKQVSDDKGFORLDSY 249
Db	251 KECHMDQDSGSNSYELSLIGCKCCTGAYVSKKNQNLISWIKQVSDDKGFORLDSY 310

ALIGNMENTS

Qy	Db
250 KFNLSILRVERVFGPGVWSTGGLETTKEVSKLDPQGVQLDVGCGIGGDFWMAENYDV	1: : : : : : : : : : : : : :
251 WLLMLYLSDOEVEDLAKKMLQWTKVGGYAFFRESCFHQSQDIIKRSKSNPHTYREPREYTKIF	1: : : : : : : : : : : : : :
252 KECHMDQDSGSNSYELSLIGCKCCTGAYVSKKNQNLISWIKQVSDDKGFORLDSY	1: : : : : : : : : : : : : :
253 F884657	311 KSSGILRVERVFGEGFVSTGGLTEPKFVMDLQDLPQGVQLDVGCGIGGDFWMAENFDV
254 T39579	310 EVVGDILSINMISFALERSIGLCAVERFVADCTKDYDPEPNSFDVYISYSDTILHQDKPA

C:Genetics:
 A:Gene: CESP:ZK622..3
 A:Introns: 34/2; 97/2; 222/3; 310/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZK622..3

Query Match 17.3%; Score 449.5; DB 2; Length 495;
 Best Local Similarity 28.6%; Pred. No. 5.6e-24; Gaps 24;
 Matches 137; Conservative 74; Mismatches 195; Indels 73; Gaps 17;

QY 12 REFKKWIHEHSYDVLTEAMMLDSQASLDKVERPEVLISMLPPEGKSVLELGAGICRFT 71
 41 RANKFSFWDKYSDDKPDNTSMMLNHSARELESSDRADITASPLBLHNKWDWJDIGAGTCRFT 100
 Db 72 GEIAKEAKSQAIVIALDFISVIKNEESINGHYKAVKFCMADVTSPSLNITSPNSVDTLISNWL 131
 101 TVLAETARWLSIDTFIDSPFIKKNRQERAHLGNNINQYQGDAV--GLKMEASNVDLFLNWL 158

QY 132 LAYLSDSERVERLVERMFKWLKGPGYIFREFRESHQS-GDHKRS-----NPTHYREPR 183
 159 MMYLSDSETEVFIFNCMHWLRSHGIGVHLRESCSEPSGRSKASKMHDNTANAMPHYRFSS 218

Db 184 FVTKLKECHMDDSGNSYELSLIGCKCIGAVKSKKNQNQSLWMLQKVDSEDD-KG-F 240
 219 LYINLLRAIRYRDVNKLWENQWSVSPYIKRSNNWQHWHWLAERKVAEDGAKGTSF 278

QY 241 QRFLD-----SSQYKENSTIERYVFGPGVSTGGLETTKEFVSKIDLKPGQ----- 287
 279 NEVLELIKNTWQNEQEAQAKDDEK-----IV-----WTDKVFESSLTSPLSNSTFLY 328

QY 288 -RVLVDYGGTGGGDFYMAENTDVEVWVGDISIMTSFALENSIGLK-CAVER----- 337
 329 TPTVTVSPYCHINA - HTIAETNNAWNTEIPEYYRTSLTKNSNNLKDQRYRFGWNQSLT 386

Db 338 -EVADCTKKDYIENSFPIVYSDTILLIQDKPALFRPHKWLKPGKLISYCKSAGTP 396
 387 DSVTYWQKD--ALFDVFEVATEFLSTVDE--TIROLPNVMSDGAKEFILEPDEVN- 439

QY 397 SAEFFAYIRQGYDLDHVAKYGKMLKDAGFVEVIAENRTDQFIQVLOKELDALEQKDD 455
 440 EAEMKQHQIQLGYTL-----KSFTDV-----TDQCIAQFQYKDHQEQLRDE 481

RESULT 5

T06795 probable 24-sterol C-methyltransferase (EC 2.1.1.41) - wheat
 N:Alternative names: delta-24-sterol methyltransferase
 C:Species: Triticum aestivum (common wheat)
 C:Accession: T06795 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 R:Subramanian, K.; Ueng, P.P.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: 215820
 A:Accession: T06795
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-363 <SUB>
 A:Cross-references: EMBL:U60754; NID:9106964; PIDN:AAB37769..1; PID:9106965

Query Match 7.9%; Score 204.5; DB 2; Length 317;
 Best Local Similarity 26.3%; Pred. No. 5.1e-07; Gaps 0;
 Matches 61; Conservative 48; Mismatches 90; Indels 33; Gaps 8;

QY 215 YVRSKKNNQNOISIWMQKVDSDEDKGQFRFLDSQYKNSIERYVFGPGVSTGGLETT 274
 35 YEKKKNFYDDSSGLWEDWGE-----HMHGYYGPHGTYRIDR-----RQAQDITI 80
 Db 275 KET-----VSKLDIKPGQKVLDVCGIGGGDFYMAENYDVEVVGIDISINMSPALE-RS 328
 81 KELLAWAVPONSAKP-RKILDLGCGIGGSSLYLAQQHQAEWVGASLSPVQVERAGERARA 139

QY 329 YGKRCAYEVADCTKKDYIENSFPIVYSDTILLIQDKPALFRPHKWLKPGKYLSD 388
 140 LGLGSTCQFOVANALDIFPASDFSDFWWSLESGEHMPNKAQFLQEAWRVWLKPGGRLLAT 199

QY 389 YC-----KSAGTPSAEFARAYIRQGYDHL-----DKAYGKMLKDAGFVEV 429
 Db 200 WCHRPIDPGNGNPLTADERRHL-QAIVDVCYLPPVSLPDEYAIARECGFGEI 250

RESULT 7

T06780 probable 24-sterol C-methyltransferase (EC 2.1.1.41) - soybean
 N:Alternative names: S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase
 C:Species: Glycine max (soybean)
 C:Accession: T06780 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 R:Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.
 J. Biol. Chem. 271, 9384-9389, 1996
 A:Title: Identification and characterization of an S-adenosyl-L-methionine: delta 24-
 A:Reference number: 215807; NID:9619190
 A:Accession: T06780
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-367 <SH1>
 A:Cross-references: EMBL:U43683; NID:91399379; PIDN:AAB04057..1; PID:91399380

Query Match 8.0%; Score 207; DB 2; Length 363;
 Best Local Similarity 28.6%; Pred. No. 4.1e-07; Gaps 8;
 Matches 68; Conservative 38; Mismatches 88; Indels 44; Gaps 8;

QY 280 KLDLKPQGKVLDVCGIGGGDFYMAENYDVEVVGIDISINMSPALE-RS 337
 114 QLBKPGMKVLDVCGIGGGLPRLARESSTSITGLNNNDYQITRGKALNRSGVGLGATCDF 173

A; Experimental source: cultivar Williams 82; etiolated hypocotyls	QY	377 WLKPGKVLIT-SDYCKSAGTSPSAFAAVIRRCYDLYKAVGKMLKDAGFVIAENRT	435
C; Superfamily: 24-sterol C-methyltransferase; bioc homology	Db	256 VLKPGGSMILHSTLAMFFGKTKNAWIDKRYIFPGGY-LPSIREVSSAMSEWFHLLAESLR	314
C; Keywords: methyltransferase; S-adenosylmethionine			
F; 122-226/Domain: bioc homology <BIOC>			
Query Match 7.4%; Score 191; DB 2; Length 367;			
Best Local Similarity 22.5%; Pred. No. 5.5e-06;			
Matches 81; Conservative 48; Mismatches 119; Indels 112; Gaps 12;			
QY 217 KSKKNQNOISWLMQKVPSEDDKGKFRT-----LDSQYKFNSLRYVERVFGPG 264	RESULT	9	
Db 3 KKKKNRNEV---WLC5AEGTGGCSRLAAMDNLASNLGGKIDKAEV LSAVQKIEY--- 53			
QY 265 YVSTGGLETTK-----ERVSK-----			
Db 54 HVCYGGQEEERKANYTDMVKNYVDDLVTSFYEGWGESPHFAPRWKGESLRESIKRHEFL 113			
QY 281 --LDLKPQKVLDVGCGIGGDFYMAENYDDEVVGIDLSTINMNSFA-LENSIGLKCVA 335			
Db 114 PLOGLKPGQKVLDVGCGIGGDFYMAENYDDEVVGIDLSTINMNSFA-LENSIGLKCVA 173			
QY 336 EFEVADCTKDYPENSFDVYIYRDTLHQDPAFLRSFSFKWIKPGKVLI-SDYCKSAG- 394			
Db 174 NFKKADFMKMPPPNSDAAVIAETCHADPAGCYKEIFRVLPGQYFAAWEWCMDSF 233			
QY 395 --TPSAFAAYTTRQGVDLHDVKAYGK--MLKDAEVEVIAER----- 434			
Db 234 DFQNPHEQKIAEELIGDGLPDIRLAKCLEARLQAGF-EV1WEDLAVDSLPLWPLD 292			
QY 435 -----TDQFQVQIQLKEDALEQKDFDIFDFSESYNDIYDGMWAKL 476			
Db 293 KSHFSLSSFRLTAVGRLFTKNAVKVL--EYVGLAPKSLRVQDFLEKAEGLVEGGKREI 350			
RESULT 8			
A81324			
Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79) Cj1183c [similarity] - Campy			
C; Species: Campylobacter jejuni			
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 24-Oct-2000			
C; Accession: A81324			
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling			
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre			
Nature, 345, 66-668, 2000			
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp			
A; Reference number: A81250; MUID:20150912			
A; Accession: A81324			
A; Status: preliminary			
A; Molecule type: DNA			
A; Residues: 1-387 <PAR>			
A; Cross-references: GB:AL139077; GB:AL11168; NID:96968444; PIDN: CAB73437.1; PID:9696861			
A; Experimental source: serotype 02, strain NCTC 1168			
C; Genetics:			
A; Gene: cfa; Cj1183c			
C; Superfamily: cyclopropane-fatty-acyl-phospholipid synthase; MCM homology			
C; Keywords: methyltransferase; phospholipid metabolism; S-adenosylmethionine			
Query Match 7.3%; Score 189.5; DB 2; Length 227;			
Best Local Similarity 35.5%; Pred. No. 5.1e-06;			
Matches 49; Conservative 25; Mismatches 53; Indels 11; Gaps 5;			
QY 257 YERVFGPGYVSTGG-----LETTKEFVSKDLPGKQVLDVGCGIGGDFYMAENYDVE 310			
Db 6 YVYRVE-PIYTIDINSQEVRSRIRTEPLIMKMKRG-KVLDLACVGQGF-F-LLELYGFE 62			
QY 311 YVYDIDSINMNSFALESIGLCAVEREYADCTKDYPENSFDVYIYRDTLHQ--DKP 368			
Db 63 YVYDIDSINMNSFALESIGLCAVEREYADCTKDYPENSFDVYIYRDTLHQ--DKP 368			
QY 369 ALERSFHKLPGKVLI 386			
Db 123 QVFKEVRVVKPSGKFIM 140			
RESULT 10			
S76226			
hypothetical protein - Synechocystis sp. (strain PCC 6803)			
C; Species: Synechocystis sp.			
A; Variety: PCC 6803			
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999			
C; Accession: S76226			
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, M.; Yama			
O, R.; Okumura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas			
DNA Res. 3, 109-136, 1996			
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys			
s. A; Reference number: S74322; MUID:97061201			
A; Status: preliminary			
A; Molecule type: DNA			
A; Residues: 1-318 <PAR>			
A; Cross-references: EMBL:D90914; GB:AB001339; NID:91653477; PIDN: BAA18485.1; PID: d101			
A; Note: the nucleotide sequence was submitted to the EMBL Data Library June 1996			
F; 94-195/Domain: bioc homology <BIOC>			
Db 197 CRRKAKERVELGLEDKIEIRLONYQDLEF-ENYFDKVSVGMFREVHGKRNGLGLYFMVKQ 255			

Query Match 7.1%; Score 195; DB 2; Length 318;
 Best Local Similarity 34.7%; Pred. No. 1.2e-05; W.D.
 Matches 42; Conservative 22; Mismatches 47; Indels 10; Gaps 2;

Qy 269 GGIETTKEFVSKUDLKDPEQKVLDVGCGGGDTYMAENYDVEVVGIDISINMISFAERS 328
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 86 GGDT-----LPPGTTVLDVGCGGGSSRLAKOYGFNTGIRISPPQVKKRATELT 136
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 329 IGLKCAVFEREVADCTKKQUPENSFDVIVSRTDTLHIDKPALFRSHWLKPGKVLD 388
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 137 -PPDVTAKFVAVDAMALSPDGSFDVWVWSVEAGPHMPKAFAKELLAKVKGILWAD 195
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 389 Y 389
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 196 W 196
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11

B75306 Query Match 7.0%; Score 195; DB 2; Length 318;
 probable cyclopropane-fatty-acyl-phospholipid synthase - Deinococcus radiodurans (strain C;Species: Deinococcus radiodurans
 C;Date: 03-DEC-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: B75306
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science, 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20056896
 A;Accession: B75306
 A;Residues: 1-462 <WHT>
 A;Experimental source: strain R1
 A;Molecule type: DNA
 A;Cross-references: GB:AE002051; GB:AE000513; NID:96459976; PIDN:AAFL1731.1; PID:9645998
 A;Keywords: SMT
 C;Genetics:
 A;Gene: DR2187
 A;Map position: 1
 C;Superfamily: cyclopropane-fatty-acyl-phospholipid synthase; MCM homology

Query Match 7.1%; Score 185; DB 2; Length 462;
 Best Local Similarity 27.7%; Pred. No. 2.5e-05;
 Matches 80; Conservative 40; Mismatches 102; Indels 67; Gaps 15;

Qy 236 DDKGQFRFLDSSQYKFNSILRVERVFGCGYVSGGLETRKE -----FVSKLDKPGQ 287
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 168 DQGAIQYHVDVSNDFYKWLDERMVNSCAYF-PGQQTLDQATAKLUDYICKRLQLRPG 226
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 288 KVLDVGCGGGDFYMAENYDVEVGIDISINMII--SPALERSIGLKCAVFEREVADCTKK 345
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 227 RLLDGGCGGGLSLYXAOHYGQVQVGLGVLSQAOQLQEGGARVVRVAGLQGQVQLEL---R 281
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 346 DYE-----NSFDVYERDTLHII--QDKPALFRSFKWLKPGKVL--ISDYCKSAG 394
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 282 DYKDWLSRKGPAQDFKIASVGMABHVGRRNMPFEYRSAYAALKPGGLMLNHAIGDIGOAR 341
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 395 TP-----SFAFAVYIQRQGVDLHDKVAKGKMLDAGFVEVIAENRRTDQFIQVQKELDALE 450
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 342 VPKWQLSQNSFA---RKYVFPD---GELLP---WETLKYSQLEFEV-RDVNL- 385
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 451 QEKDDFIDDFSEBDIYDVGKAKL-----VTTCEEQQ --WGLFI 490
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 386 -----REHYAHLTIGHWAARLEAHRPERALLGEERLRLWRLYL 423
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12

T01572 Query Match 7.0%; Score 182; DB 2; Length 344;
 Best Local Similarity 25.7%; Pred. No. 2.2e-05;
 Matches 61; Conservative 41; Mismatches 93; Indels 42; Gaps 7;

Qy 280 KLDIKPGOKVLDVGCGGGDFYMAENYDVEVGIDISINMISFA--LERSIGLKCAVEF 337
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 95 QLQIKPGMVKVLDVGCGTGGPLREIARFSSTSVTGNNNEYQITRGKELNRLAGISGCDP 154
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 338 EVADCTKKDYPENSFDVIVSRTDTLHIDKPALFRSHWLKPGKVLDIC-KSAGTP 396
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

C;Accession: T01572
 R;Tong, Y.; Nes, W.D.
 submitted to the EMBL Data Library, January 1998
 A;Reference number: Z14350
 A;Accession: T01572
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-344 <WHT>
 A;Cross-references: EMBL:AF045570; NID:92909845; PIDN: AAC04265.1; PID:92909846
 A;Experimental source: strain B73
 A;Genetics:
 A;Gene: SMT
 C;Superfamily: 24-sterol C-methyltransferase; bioc homology
 C;Keywords: methyltransferase; S-adenosylmethionine
 F;101-205/Domain: bioc homology <BIOC>

Query Match 6.8%; Score 177; DB 2; Length 348;
 Best Local Similarity 27.6%; Pred. No. 4.9e-05; Gaps 8;
 Matches 54; Conservative 32; Mismatches 62; Indels 48; Gaps 8;

Qy 223 NQISWLMOKV-----DSE--DDKGFO---RFLOSSQKFNSILRYERYFGP 263
 Db 69 NETSGLMWEIWMGDMMHGFYDPDSSVQLSDSGHKEAQTRMIES-----LRFAGV--- 118

Qy 264 GVVSTGGLETTKEFVSKLDLKGQKVLGVGGCGGGDFYMAENYDVEVVGIDLSINMISF 323
 Db 119 -----TDEEEIGKLT-----KVVVDGCCIGGSSRYLASKFGARCIGILSLPVQAKR 164

Qy 324 A---LERSIGLCAVEFADCTRKDPYENSDVYISRTDILHQDQKPALFRSFHKWLKPG 381
 Db 165 ANDLAAOSLAHKASFQVADALDQPFEDGKFELWMSMEGERIMPDKAKFKVKEVLRVVAAPG 224

Qy 382 GKVLSIISDYCK---SAG 394
 Db 225 GRILIVIWCHRNLSLAG 240

RESULT 15
 S18533

eryG protein - *Saccharopolyspora erythraea*
 C;Species: *Saccharopolyspora erythraea*
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 22-Oct-1999
 C;Accession: S18533; S16747
 R;Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.
 Mol. Gen. Genet. 230, 120-128, 1991
 A;Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in methytransferases.
 A;Reference number: S18530; MUD:92079886
 A;Accession: S18533
 A;Molecule type: DNA

RESULT 14
 S96673

gamma-tocopherol methyltransferase [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: C96673

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Ruiz, L.; Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maili, R.; Marziali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A06141; MUID:21016719

A;Accession: C96673

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-348 <STO>

A;Cross-references: GB:AE005173; NID:98099780; PIDN:AAD38271.2; GSPDB:GN00141

A;Genes: F13011.27

A;Map position: 1

Query Match 6.8%; Score 176.5; DB 2; Length 306;
 Best Local Similarity 27.8%; Pred. No. 4.3e-05; Gaps 9;
 Matches 60; Conservative 36; Mismatches 81; Indels 39; Gaps 9;

Qy 264 GYVSTG--GL-ETTKFVSKL---DIKPGQKVLDVGCGGGDFYMAE-NYDVEVVGID 315
 Db 53 GYWKPGCAGLEANQELAQNAEAGAISSEGDEVILVFGGLAQADFVLETRPARIVGD 112

Qy 316 LSINMISALERS--IGLKCAVEFVADCTKKYDPEPENSFDVYISRDTHLTDQKPLFRS 373
 Db 113 LTPSHVRVIRASERAERENVQDRLQFKEGSATDIFPFGAETFRVTSLESALHWRPRTDFKG 172

Qy 374 FHRWLKGQGKVLISDYCK-----SAGTPSAEFAAVYRQRYDH-----DVKAY 417
 Db 173 AFEVTLPGVGLAEGDIPDRLRPGSDQCPKK----LAPQRGSLSGQIPVENVWPREY 227

Qy 418 GKMILKDGAEV-----IAENRTDQFIQVKE 445
 Db 228 AKQLRLRAGFVDVEVKSYRDNVMEPWLDWLRKLODE 263

Search completed: September 20, 2001, 16:20:09
 Job time: 167 sec

A;Residues: prel_imary

A;Cross-references: GB:AE005173; NID:98099780; PIDN:AAD38271.2; GSPDB:GN00141

A;Genes: F13011.27

A;Map position: 1

Query Match 6.8%; Score 177; DB 2; Length 348;
 Best Local Similarity 27.6%; Pred. No. 4.9e-05; Gaps 8;
 Matches 54; Conservative 32; Mismatches 62; Indels 48; Gaps 8;

Qy 223 NQISWLMOKV-----DSE--DDKGFO---RFLOSSQKFNSILRYERYFGP 263
 Db 69 NETSGLMWEIWMGDMMHGFYDPDSSVQLSDSGHKEAQTRMIES-----LRFAGV--- 118

Qy 264 GVVSTGGLETTKEFVSKLDLKGQKVLGVGGCGGGDFYMAENYDVEVVGIDLSINMISF 323
 Db 119 -----TDEEEIGKLT-----KVVVDGCCIGGSSRYLASKFGARCIGILSLPVQAKR 164

Qy 324 A---LERSIGLCAVEFADCTRKDPYENSDVYISRTDILHQDQKPALFRSFHKWLKPG 381
 Db 165 ANDLAAOSLAHKASFQVADALDQPFEDGKFELWMSMEGERIMPDKAKFKVKEVLRVVAAPG 224

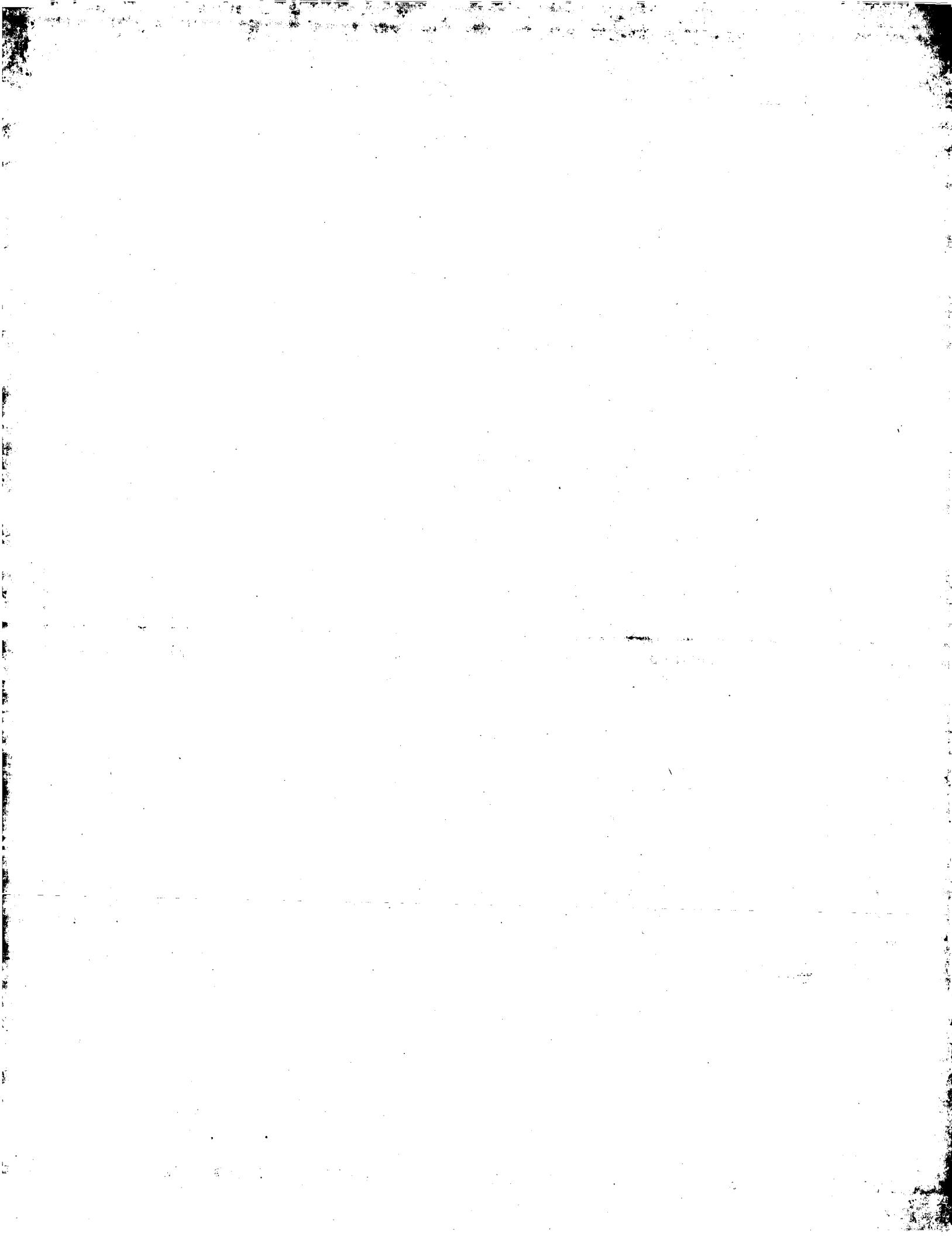
Qy 382 GKVLSIISDYCK---SAG 394
 Db 225 GRILIVIWCHRNLSLAG 240

RESULT 15
 S18533

eryG protein - *Saccharopolyspora erythraea*
 C;Species: *Saccharopolyspora erythraea*
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 22-Oct-1999
 C;Accession: S18533; S16747
 R;Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.
 Mol. Gen. Genet. 230, 120-128, 1991
 A;Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in methytransferases.
 A;Reference number: S18530; MUD:92079886
 A;Accession: S18533
 A;Molecule type: DNA

A;Residues: 1-306 <HAY>
 A;Cross-references: EMBL:X60379; NID:948941; PIDN:CAA42929.1; PID:9581650

A;Genetics:
 A;Gene: eryG
 A;Start codon: GRG
 A;Superfamily: bioc homology
 F;82.187/Domain: bioc homology <BIOC>



Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5		
Run on:	September 20, 2001, 16:19:23 : Search time 14.71 seconds (without alignments)		
OM protein - protein search, using sw model	1150.388 Million cell updates/sec		
Title: US-09-525-885-2	Perfect score: 2598		
Sequence: 1 MAA\$AMVQI\$QEREVFKK\$WI..... KLYV\$TE\$EQ\$QWGL\$FI\$AK\$M 494			
Scoring table: BLOSUM62			
Gapop 10.0 , Gapext 0.5			
Searched: 93435 seqs, 3255486 residues			
Total number of hits satisfying chosen parameters: 93435			
Minimum DB seq length: 0			
Maximum DB seq length: 200000000			
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries			
Database : SwissProt; 39;*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	176	6.8	381 1 CFA_ECOLI
2	170	6.5	P25087 escherichia
3	161.5	6.2	P25087 saccharomy
4	148.5	5.7	014321 schizosacch
5	144	5.5	074198 candida alb
6	144	5.5	P46326 bacillus su
7	135.5	5.2	P28511 escherichia
8	135	5.2	P20187 streptomyce
9	142.8	5.2	086169 bacillus st
10	142.8	4.9	P49016 lactococcus
11	128	4.9	P17993 escherichia
12	127.5	4.9	P08442 synochococc
13	126	4.8	P37431 salmonella
14	123.5	4.8	055423 synochocyst
15	123	4.7	P25397 escherichia
16	120	4.6	Q37060 haemophilus
17	119	4.6	P44074 haemophilus
18	118.5	4.6	P35337 neurospora
19	117.5	4.5	P44548 bacillus su
20	117.5	4.5	059534 pyrococcus
21	117	4.5	P31049 pseudomonas
22	116.5	4.5	P36571 serretia ma
23	115	4.4	P063159 r hexapreny
24	115	4.4	Q11195 mycobacteri
25	114.5	4.4	Q11196 mycobacteri
26	113.5	4.4	P54289 homo sapien
27	112	4.3	P13806 oryctolagus
28	111	4.3	Q05972 rickettsiae
29	110.5	4.3	Q01500 p genome po
30	110	4.2	P47729 mycoplasma
31	110	4.2	P033392 mycobacteri
32	109.5	4.2	P54290 rattus norv
33	109.5	4.2	P46208 bacillus su
1	699	1 HS83_ARATH	CC
ALIGNMENTS			
RESULT 1	ID CFA_ECOLI	STANDARD;	PRT; 381 AA.
RP	RP30010;		
RC	DT 01-APR-1993 (Rel. 25, Created)		
RC	DT 01-APR-1993 (Rel. 25, Last sequence update)		
RC	DT 01-NOV-1997 (Rel. 35, Last annotation update)		
RC	DE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)		
RC	DE CYCLOPROPANE FATTY ACID SYNTHASE (CFA SYNTHASE).		
RA	RA CFA OR CDFA.		
RA	RA Wang A.-Y., Grogan D.W., Cronan J.E. Jr.;		
RA	RA Escherichia coli.		
RA	RA Bacteriad; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
RA	RA Escherichia; Proteobacteria; Enterobacteriaceae;		
RA	RA NCBI_TaxID=562;		
RA	RA RN [1] SEQUENCE FROM N.A., SEQUENCE OF 1-8, AND CHARACTERIZATION.		
RA	RA RN STRAIN=K12;		
RA	RA RN MEDLINE=93015691; Pubmed=1445840;		
RA	RA RN Wang A.-Y., Grogan D.W., Cronan J.E. Jr.;		
RA	RA RN "Cyclopropane fatty acid synthase of Escherichia coli: deduced amino acid sequence, purification, and studies of the enzyme active site.";		
RA	RA RN Biochemistry 31:11020-11028(1992).		
RA	RA RN [2] SEQUENCE FROM N.A.:		
RA	RA RN STRAIN=K12 / RR28;		
RA	RA Eberhardt S.M.R., Richter G., Gimbel W., Werner T., Bachner A.;		
RA	RA RN Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.		
RA	RA RN [3] SEQUENCE FROM N.A.:		
RA	RA RN STRAIN=K12 / MG1655;		
RA	RA MEDLINE=97426617; Pubmed=9278503;		
RA	RA Blattner F.R., Plunkett G. III, Bloch C.A., Perera N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Matthew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,		
RA	RA RA Mau B., Shao Y.;		
RA	RA "The complete genome sequence of Escherichia coli K-12.";		
RA	RA Science 277:1453-1474(1997).		
RA	RA RN [4] SEQUENCE FROM N.A.		
RA	RA RC STRAIN=K12;		
RA	RA RX MEDLINE=97251357; Pubmed=9097039;		
RA	RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kassi H., Kashimoto K., Kimura S., Kitakawa M., Makino K., Mikuni T., Miyobuchi K., Mori H., Mori T., Kitagawa M., Makino K., Mikuni T., Miyobuchi K., Mori H., Mori T., Oshima T., Saito N., Sampai G., Seki Y., Sivasundaram S., Tagami H., Takeeda J., Takekoto K., Takeuchi Y., Wada C., Yamamoto H., Horuchi T.		
RA	RA RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map"; DNA Res 3:363-377(1998).		
CC	CC -1- FUNCTION: TRANSFERS A METHYLENE GROUP FROM S-ADENOSYL-L-METHIONINE TO THE CIS DOUBLE BOND OF AN UNSATURATED FATTY ACID CHAIN		
CC	CC RESULTING IN THE REPLACEMENT OF THE DOUBLE BOND WITH A METHYLENE BRIDGE.		
CC	CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + PHOSPHOLIPID		

CC OLEFINIC FATTY ACID = S-ADENOSYL-L-HOMOCYSTEINE + PHOSPHOLIPID

CC CYCLOPROPANE FATTY ACID.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -----

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CC -----

CC EMBL: M98330; AAA23562.1; -.

DR EMBL; X91109; -; NOT_ANNOTATED_CDS.

CC "Mutations in L131 (ERG6) gene confer increased sodium and lithium uptake in *Saccharomyces cerevisiae*." [3]

CC EMBL; A000261; AAC74733.1; -.

DR EMBL; D50809; BAA15428.1; -.

DR EMBL; D50810; BAA15437.1; -.

DR PIR: A44292; A44292

ECO:Gene; EG11531; cfa.

PFam: PF00972; Flvi_N55; 1.

DR Transf erase; Methyltransf erase; Lipid synthesis.

FT INITI_MET 0 1 S -> R (IN REF 2).

FT CONFLICT 7 7 E -> G (IN REF 2).

FT CONFLICT 24 24 S -> N (IN REF 2).

FT CONFLICT 38 38 I -> T (IN REF 2).

FT SEQUENCE 381 AA; 43777 MW; 1F07B220C7E088ADF CRC64;

CC -----

CC Query Match 6.8%; Score 176; DB 1; Length 381; Best Local Similarity 29.3%; Pred. No. 1.2e-05; Mismatches 65; Conservative 27; Indels 50; Gaps 12; Matches 65; Conservative 27; Mismatches 80; Indels 50; Gaps 12;

CC -----

CC QY 184 FVTKIFK-----ECHMQDDSGNSYELSLIGCKCIGAVYKSKKNQNOISWLMQKVSEED 236

DR 74 FFSKVLRAGLENOLPHFRKD-----TLRIAGARLFN--LQSKKR---AWLVGK--EHY 119

DR 237 DKG--FORFLDSSQYKFNISLRLRVERVFGPGYVSTGGLETT---KEFVSKIDLKPQCK 288

DR 120 DQGLNDLPSMRD-----PEMOMSCAT--WKAQDADNEAQAKLNMCEKQLKGMR 169

DR 289 VLDVGCGGGDFYMAENNDEVVGIDISINMSFALERSIGKCAVFEVADCTKKDYP 348

DR 170 VLDIGGCGGNGLALYMASWIDSVWGVITISAEQOKMAQRCGEGLDVTIILQ-----DVR 222

DR 349 E--NSFDIVYTSRDTLHQDK--PALFHSFHKWLKPGCKVLI 386

DR 223 DLNDQFDKIVSVGMFERVGPKKNYDTYFAVWDRNLKPEGIFLL 264

CC -----

CC DR PIR: SL2003; S42003.

DR SWISS-2DPAGE; P25087; YEAST.

DR YEPD; 6410; -.

-DR SGD; S0004467; ERG6.

DR KW Sterol biosynthesis; Transferase; Methyltransferase; Acetylation.

DR FT INITI_MET 0 0 MOD_RES 1 1

DR FT CONFLICT 379 379 E -> EE (IN REF 2).

DR FT SEQUENCE 382 AA; 43299 MW; D76BAE9E3D9C7D71B CRC64;

CC -----

CC Query Match 6.5%; Score 170; DB 1; Length 382; Best Local Similarity 23.6%; Pred. No. 3.2e-05; Mismatches 65; Conservative 44; Indels 40; Gaps 9; Matches 65; Conservative 44; Mismatches 127; Indels 40; Gaps 9;

CC -----

CC QY 190 KECHMQDDSGNSYELSLIGCKCIGAVYKSKKNQNO--ISWLMQKVSEDDKG--- 239

DR 14 REH-GDDIGKKTGLSAL-----MSKNNSAQEAVQVQLRNWDGRTDKAERRLE 63*

DR 240 -----FORFLDSSQYKFNISLRLRVERVFGPGYVSTGGLETTKVEVS-KIDLKPQCK 289

DR 64 DYNEATHSYVNVVTFYEGWGSFFHSR-FYKGESFAASTARHAEYLAVKAGIQDLY 122

DR 290 LDVGCGGGDFYMAENNDEVVGIDISINMSFALERSIGKCAVFEVADCTKKDY 347

DR 123 LDVGCGGGDFYMAENNDEVVGIDISINMSFALERSIGKCAVFEVADCTKKDY 347

DR 348 PENSFDIVYTSRDTLHQDKPALFRSHKWLKPGCKVLIISDYCKS---AGTPSAFAAY 403

DR 183 EENTFDKVIAEATCCHAPKLEGVYSEIYKVLPGGTAVVWMTKYDENPNPEHKKIAY 242

CC -----

CC MEDLINE-94312403; PubMed=8038180;

CC -----

CC RA Weihinda A.A.; Beavis A.D.; Trumbly R.J.; RT "Characterization of PR4, a *Saccharomyces cerevisiae* gene that confers pleiotropic drug resistance in high-copy number: identity with YAP1, encoding a transcriptional activator." [4]

CC RA Gentiles S.; Bowman S.; Barrell B.G.; Rajandream M.A.; Walsh S.V.; RT Submitted S. (JUN-1995) to the EMBL/GenBank/DBJ databases.

CC RL Biochim. Biophys. Acta 1193:107-117(1994).

CC RL [3]

CC SEQUENCE FROM N.A.-----

CC RA Hussain M.; Lenard J.; Garrels J.I.; Fletcher B.; Kobayashi R.; Latter G.I.; Schwender B.; Volpe T.; Warner J.R.; McLaughlin C.S.; RT Submitted (SEP-1994) to the SWISS-PROT data bank.

CC CC -----

CC CC -1- FUNCTION: METHYLTRANSFERASE REQUIRED FOR ERGOSTEROL SYNTHESIS.

CC CC 8,24-DIEN-3-BETA-OL = S-ADENOSYL-L-HOMOCYSTEINE + 24-METHYLENE-5-ALPHA-CHOLEST-8-EN-3-BETA-OL.

CC -----

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CC -----

CC DR EMBL: X74249; CA052308.1; -.

DR EMBL; 249810; CAR09944.1; -.

DR EMBL; X53830; CAA37826.1; -.

DR PIR: PE0402; PE0402.

DR PIR: S17001; S17001.

DR PIR: S33982; S35982.

DR PIR: SL2003; S42003.

DR SWISS-2DPAGE; P25087; YEAST.

DR YEPD; 6410; -.

-DR SGD; S0004467; ERG6.

DR KW Sterol biosynthesis; Transferase; Methyltransferase; Acetylation.

DR FT INITI_MET 0 0 MOD_RES 1 1

DR FT CONFLICT 379 379 E -> EE (IN REF 2).

DR FT SEQUENCE 382 AA; 43299 MW; D76BAE9E3D9C7D71B CRC64;

CC -----

CC Query Match 6.5%; Score 170; DB 1; Length 382; Best Local Similarity 23.6%; Pred. No. 3.2e-05; Mismatches 65; Conservative 44; Indels 40; Gaps 9; Matches 65; Conservative 44; Mismatches 127; Indels 40; Gaps 9;

CC -----

CC QY 190 KECHMQDDSGNSYELSLIGCKCIGAVYKSKKNQNO--ISWLMQKVSEDDKG--- 239

DR 14 REH-GDDIGKKTGLSAL-----MSKNNSAQEAVQVQLRNWDGRTDKAERRLE 63*

DR 240 -----FORFLDSSQYKFNISLRLRVERVFGPGYVSTGGLETTKVEVS-KIDLKPQCK 289

DR 64 DYNEATHSYVNVVTFYEGWGSFFHSR-FYKGESFAASTARHAEYLAVKAGIQDLY 122

DR 290 LDVGCGGGDFYMAENNDEVVGIDISINMSFALERSIGKCAVFEVADCTKKDY 347

DR 123 LDVGCGGGDFYMAENNDEVVGIDISINMSFALERSIGKCAVFEVADCTKKDY 347

DR 348 PENSFDIVYTSRDTLHQDKPALFRSHKWLKPGCKVLIISDYCKS---AGTPSAFAAY 403

DR 183 EENTFDKVIAEATCCHAPKLEGVYSEIYKVLPGGTAVVWMTKYDENPNPEHKKIAY 242

CC -----

CC MEDLINE-94312403; PubMed=8038180;

Db 270 VGFE--IYQKD-LADVDE 286
 RESULT 5
 YBB_BACSU STANDARD; PRT; 244 AA.
 AC P46326; 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 28.2 KDA PROTEIN IN ALDX-ASN1 INTERGENIC REGION.
 GN YBB OR VETCR.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Staphylococcus group; Bacillus.
 OC NCBI_TAXID=1423;
 [1] SEQUENCE FROM N.A.
 RC STRAIN=168 / BGSC1A1;
 RX MEDLINE=96093926; PubMed=7584049;
 RA Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;
 RT "Cloning and sequencing of a 36-kb region of the *Bacillus subtilis*
 genome between the *gnt* and *iol* operons.";
 RL 2,61-69(1995).
 CC -- SIMILARITY: TO E.COLI YAFE.
 CC -- SIMILARITY: TO METHYLTRANSFERASES.
 CC --
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 or send an email to license@isb-sib.ch).
 CC --
 CC EMBL; AB00554; BAA21596.1; -.
 DR EMBL; 299124; CAB16025.1; -.
 DR InterPro; IPR000339; -.
 DR InterPro; IPR000339; -.
 DR Pfam; PF01209; Ubie.methyltran; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 244 AA; 28222 MW; 5B008371AFD3D02B CRC64;
 CC Query Match 5.5%; Score 144; DB 1; Length 244;
 CC Best Local Similarity 20.4%; Pred. No. 0.0013; Gaps 8;
 CC Matches 55; Conservative 49; Mismatches 118; Indels 48;
 CC Gaps 8;
 QY 232 VDSEDDKGFRFLDSSQYKFNSTL--RYVERFGPGYVSTGGLETKEFVSKLDKPGQKV 289
 DB 2 ITAECKTYKERVLDLQSYLPLGARLSRMSPP----- -KNKVI 40
 QY 290 LDVGCGIGGDFYMAENYDVEVVGIDLSINMISFALE--RSIGLKCAVEFEVADCKKDY 347
 DB 41 IDMGTTGPGYLSQLAKRINAHVAVDNPAMHEIAQEAKSGVSSLISFDLEDVHLSY 100
 QY 348 PENSDFWYISRTILHQDQPKALFRSHFWKWLPGKGLSYQCKSAGT-----PSA 398
 DB 101 ADQYADFIVSYSLHNDWVKGKLCYRVLAPGKIVLDFNPOGSHLIMRKOKEP 160
 QY 399 EFAAYR--ORGYLDHVKAQGMKMDAGFVEVIAFN--RTDQITQVQLEKDALEQ 452
 DB 161 EYFVFVREAFESYSSEFDIHQF--YDAGIPNYSLETFHFLPDEFIESDELEDAPLW 217
 QY 453 KDDFIDDFSEEDYNDIVDGWKAQKLVRITQE 482
 DB 218 QNDQSTDHEIESVT----WMLTIEKEKEG 242
 DR 01-AUG-1992 (Rel. 23, Created)
 DR 15-JUL-1998 (Rel. 36, Last sequence update)
 DR 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UBIQUINONE/MENAQINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE
 DE (EC 2.1.1.-).
 GN OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TAXID=562;
 [1] RN SEQUENCE FROM N.A.
 RP RC STRAIN=K12 / MG1655;
 RX MEDLINE=92350234; PubMed=1379743;
 RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.,
 RT "Analysis of the *Escherichia coli* genome: DNA sequence of the region
 from 84.5 to 86.5 minutes.";
 RL Science 257;71-778(1992).
 RN [2] RP REVISION TO 101.
 RC RX STRAIN=K12 / MG1655;
 RX MEDLINE=97456617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RL Riley M., Collado-Vides J., Glaser J.D., Rode C.K., Ma N, Graw G.F.,
 RA Gregor J., Davis N.W., Kirpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT RN "The complete genome sequence of *Escherichia coli* K-12.";
 RT RN [3] RP CHARACTERIZATION, AND VARIANT UBIE401.
 RX MEDLINE=97197541; PubMed=9045837;
 RA Lee P.T., Hsu A.Y., Ha H.-Y., Clarke C.F.;
 RT "A C-methyltransferase involved in both ubiquinone and menaquinone
 biosynthesis: isolation and identification of the *Escherichia coli*
 ubie gene."
 RL J. Bacteriol. 179:1748-1754(1997).
 CC --
 CC -!- FUNCTION: CONVERTS DDMH2 INTO DMQH2 AND DMKH2 INTO MKH2.
 CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 2-POLYPRENYL-6-
 CC METHOXY-1,4-BENZOQUINOL = S-ADENOSYL-L-HOMOCYSTEINE + 2-
 CC POLYPRENYL-3-METHYL-6-METHOXY-1,4-BENZOQUINOL.
 CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DEMETHYLMENAQINOL =
 CC S-ADENOSYL-HOMOCYSTEINE + MENAQINOL.
 CC -!- PATHWAY: INVOLVED IN BOTH UBIQUINONE AND MENAQINONE BIOSYNTHESIS.
 CC -!- SIMILARITY: BELONGS TO THE UBIE FAMILY.
 CC --
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 or send an email to license@isb-sib.ch).
 CC --
 CC EMBL; AB00459; AAC76836.1; -.
 DR PIR; SS0722; S30722.
 DR Ecogene; EG11473; ubie.
 DR InterPro; IPR000339; -.
 DR Pfam; PF01209; Ubie.methyltran; 1.
 DR PROSITE; PS01183; UBIE_1; 1.
 DR PROSITE; PS01184; UBIE_2; 1.
 DR PROSITE; PS01185; UBIE_3; 1.
 KW Menaqinone biosynthesis; Ubiquinone biosynthesis; Transferase;
 KW Methyltransferase.
 FT VARIANT 142 G -> D (IN UBIE401 ALLELE, DEFECTIVE).
 FT CONFLICT 101 101 P -> L (IN REF. 1).
 SQ SEQUENCE 251 AA; 28057 MW; 646FEB09A0075AE CRC64;
 CC Query Match 5.5%; Score 144; DB 1; Length 251;
 CC Best Local Similarity 26.8%; Pred. No. 0.0014; Gaps 7;
 CC Matches 52; Conservative 36; Mismatches 88; Indels 18; Gaps 7;

RESULT 6
 UBIE_ECOLI UBIE_ECOLI STANDARD; PRT; 251 AA.
 AC P27851;

RESULT	7	STANDARD;	PRT;	345 AA.
YT37_STRFR	YT37_STRFR			
AC P2018;		P2018; 1991 (Rel. 17, Created)		
DT 01-FEB-1991 (Rel. 17, Last sequence update)				
DT 15-JUL-1999 (Rel. 38, Last annotation update)				
DE HYPOPOHETICAL PROTEIN IN TRANSPOSON TN4556.				
OS Streptomyces fradiae.				
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;				
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
OC NCBI_TaxID=1906;				
RN [1]				
RP SEQUENCE FROM N.A., AND FUNCTION.				
RC STRAIN=ATCC 10149;				
RX MEDLINE=97284706; PubMed=9139683;				
RA Koike-Takeshita A., Koyama T., Ogura K.;				
RT "Identification of a novel gene cluster participating in menaquinone (menaquinin K2) biosynthesis. Cloning and sequence determination of the 2-heptaprenyl-1,4-naphthoquinone methyltransferase gene of <i>Bacillus stearothermophilus</i> ."				
RT J. Biol. Chem. 272:12280-12383 (1997).				
CC -I- FUNCTION: CONVERTS DMK12 INTO MK12.				
CC -I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DEMETHYLMENAQUINOL = S-ADENOSYL-L-HOMOCYSTEINE + MENAQUINOL.				
CC -I- PATHWAY: LAST STEP IN MENAQUINONE BIOSYNTHESIS.				
CC -I- SIMILARITY: BELONGS TO THE UBIE FAMILY.				
CC				
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CC				
CC EMBL; D87054; BA32500.1; -.				
CC DR InterPro; IPR00339; -.				
CC DR Pfam; PF01208; Ubie_methyltran; 1.				
CC DR PROSITE; PS01183; UBIE_1; 1.				
CC DR PROSITE; PS01184; UBIE_2; FALSE_NEG.				
CC KW Metaquinoine biosynthesis; transFerase; Methyltransferase.				
CC SO SEQUENCE 234 AA; 27128 MW; 8C1CDA06A25F953 CRC64;				
CC				
DR EMBL; M29297; AAA88564.1; -.				
DR PIR; J00429; J00429.				
DR InterPro; IPR000339; -.				
DR Pfam; PF01208; Ubie_methyltran; 1.				
DR Hypothetical protein; Transferase; Methyltransferase;				
DR Transposable element; Transferase; Methyltransferase;				
DR SEQUENCE 345 AA; 37113 MW; 027CDA5B3F8AA7CC CRC64;				
DR				
DR Query Match 5.2%; Score 135.5; DB 1; Length 234; Best Local Similarity 21.9%; Pred. No. 0.0057; Mismatches 80; Indels 46; Gaps 7; Matches 47; Conservative 42; Mismatches 80; Indels 46; Gaps 7;				
DR				
DR QY 246 SSQY-KFNSILRYVERVFGPGVYVSTGPLETKEFVSKDLPKGQKVLDVGCGIGGGDFYMA 304				
DR Db 17 SAHYDRMNSVISFRR-----HLWKRKDVNRMRMVKQGKALDVCCGTADWTTIALA 66				
DR				
DR QY 305 ENIDVE--VVGIDLISINNISFALE--RSIGLKAVEREVAEDCTKKDYPENSIVIISRTD 360				
DR Db 67 EAVGPESKRYVGDFSENMLVKGEQKVKARGLH-NVKLJHGNAMQLPDPNSDSDYVITGFG 125				
DR				
DR QY 361 TIHQDKPALKFSPFKWNLKPGGVVLSDYCKSAGPT----- 396				
DR				
DR 126 LRNVPDVMTVLMKEMHRTYKPGGTVV--CLETSQLPILFGFRQLVYFYFREIMPLGKLL 181				
DR				
DR QY 397 --SAEFAAYIRQGYDLHDVKAYGKMLKDAFGEVY 429				
DR				
DR 182 AKSYEYSWLQBSAREFPGRDELAMFRAAGFVVD 216				
DR				
DR RESULT 9				
DR GRCB_LACLA				
DR ID GRCB_LACLA STANDARD;				
DR AC P09016;				
DR DT 01-FEB-1996 (Rel. 33, Last sequence update)				
DR DT 01-FEB-1996 (Rel. 33, Last sequence update)				
DR				
DR 241 -----PDLEVS-----RAYTRHVDKIVRNGVIGRQLARLALDAGF 276				
DR				
RESULTS 8				

AC Q55423;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PURINE METHYLTRANSFERASE SLU0829 (EC 2.1.1.-).
 GN SLU0829.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TAXID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RT SEQUENCE FROM N.A.
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugiyama M., Tabata S.;
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 648 to 928 of the genome.";
 RL DNA Res. 2;153-156(1995).
 CC -1- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY.
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 CC
 DR EMBL; D64003; BAA10522.1; -.
 DR InterPro; IPR000339; -.
 DR Pfam; PF01209; Ubiquitinyltran; 1.
 DR Hypothetical protein; Methyltransferase.
 KW SEQUENCE 212 AA; 23071 MW; BAD77E2E605A7001 CRC64;
 SQ

Query Match 4.8%; Score 126; DB 1; Length 212;
 Best Local Similarity 27.7%; Pred. No. 0.022; DB 1;
 Matches 54; Conservative 32; Mismatches 77; Indels 32; Gaps 12;
 QY 266 VSGVGGLETFK-VSKLUDKPGSKQVLDVGCGGKGDFYMAENYDVEVYGDLSINMISFA 324
 DB 25 LNVGGEERPHDLDENLAISPGKVLQDCCGGQQATVLAQS-GATVWGLDAS----- 76
 QY 325 LERSIGLKCVAEEFVADCT-----KKDYP--EENSDVIVSRTQTLHTQDKPAFLRSP-- 374
 DB 77 -PKALG--RAKINVPQTGYVQGLAEIDLPLFGEGEFDLVHT-SVALH-EMTPAQOLISG 130
 QY 375 -HWWLKGPGKVILSYDCKSAG---TSAEF-AAVYIQRGYDILHDVAKYGMKMKDAGFVE 428
 DB 131 VHRVLRKGFGIFALWLRPSNMWFWPPLAIFMGLFETETAWOLINTD-LGSLLDQAGFTV 189
 QY 429 VTAENRTDFOIQLQ 443
 DB 190 VRKHLIYAGGSLQVHQ 204

RESULT 14
 ID TEHB_ECOLI
 AC P25397; P76066; STANDARD; PRM; 197 AA.
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TEHLURITE RESISTANCE PROTEIN TEHB.
 GN
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OX Escherichia;
 RN NCBI_TAXID=562;
 RP [1]
 SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97420617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN=K12;
 RX MEDLINE=9751357; PubMed=9097039;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampai G., Seki Y., Sivasundaram S.,
 RA Tagami H., Takeeda J., Takeuchi K., Wada C.,
 RA Yamamoto Y., Horiochi T.;
 RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [4]
 RP GENE MAPPING.
 RC STRAIN=K12;
 RX MEDLINE=9422856; PubMed=8169225;
 RA Taylor D.E., Hou Y., Turner R.J., Weiner J.H.;
 RT "location of a potassium tellurite resistance operon (tehA tehB)
 within the terminus of Escherichia coli K-12.";
 RL J. Bacteriol. 176:2740-2742(1994).
 CC -1- FUNCTION: RESPONSIBLE FOR POTASSIUM TELLURITE RESISTANCE WHEN
 PRESENT IN HIGH COPY NUMBER, PROBABLY BY INCREASING THE REDUCTION
 CC RATE OF TELLURITE TO METALLIC TELLURUM WITHIN THE BACTERIUM.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE PLASMID ENCODED.
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 CC
 DR EMBL; M74072; AA119564.1; -.
 DR EMBL; AE000240; AAC74512.1; -.
 DR EMBL; D90782; BAA15050.1; -.
 DR PIR; JQ1018; JQ1018.
 DR Ecogene; EG11884; tehb.
 DR Antibiotic resistance; Tellurite resistance.
 KW SEQUENCE 197 AA; 22531 MW; BF0D2D64FB9C2B8 CRC64;
 SQ

Query Match 4.8%; Score 123.5; DB 1; Length 197;
 Best Local Similarity 28.6%; Pred. No. 0.031; DB 1;
 Matches 59; Conservative 29; Mismatches 83; Indels 35; Gaps 13;
 QY 254 ILRVERVFGPGVSTGGLETTEKFVSKLD-LKPGQKVLDVGCGGIGGDFYMAEN-YDVEV 311
 DB 2 LIRDENYFTDKELT--RTTSEVLEVKVVKPG-KTLDIGCGGRNSLYLAAANGYDVA 57
 QY 312 VGDLSINMISFA-LER--SIGLKCVAEEFVADCTKKDYPNSFDVIVSRTQTLHTQDK- 367
 DB 58 --WDKNAMSTANVERIKSESENLDNHLHTRYVLDNLTF-DQYDFILSTVVLMLEAKT 112
 RX MEDLINE=91285417; PubMed=2060788;

QY 368 -PALFRSHKWLKPGGVLI-----SDYCKSAGTPSAEFAAYIRO----RGY----- 409

Job time: 123 sec

Search completed: September 20, 2001, 16:21:26

GenCore version 4.5
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OM protein - protein search, using sw model
 Run on: September 20, 2001, 16:18:13 ; Search time 19.82 Seconds
 (without alignments)
 3297.613 Million cell updates/sec

Title: Perfect score: US-09-525-885-2
 Sequence: 1 MASAMGVQLQEREFVKKWIEHSVDTLVEAMMLDSASLDKVERPEVLSMPPYEGKSV 694
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPREMBL_16:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2598	100.0	494	10	Q9M571 spinacia ol
2	2105.5	81.0	491	10	Q9FR44 arribidopsis
3	2093.0	80.6	498	10	Q9LVB3 arribidopsis
4	1287.5	49.6	374	10	Q9LP63 arribidopsis
5	767.5	29.5	180	10	Q9LP64 arribidopsis
6	498.5	19.2	437	5	Q22993 caenorhabdi
7	494.5	17.3	495	5	Q23552 caenorhabdi
8	223	8.6	565	2	Q9KJ20 actinopolys
9	207	8.0	363	10	Q41586 triticum ae
10	207	8.0	363	10	Q41587 triticum ae
11	204.5	7.9	317	2	Q55809 synchocyst
12	199	7.7	278	2	Q8EY12 streptomyce
13	196	7.5	346	10	Q82720 niicotiana t
14	193.5	7.4	279	2	Q9KJ21 ectothiorho
15	191	7.4	367	10	Q43445 glycine max
16	189.5	7.3	275	2	Q9X5Q8 streptomyce
17	189.5	7.3	283	2	Q9X5Q9 streptomyce
18	189.5	7.3	387	2	Q9Pb2 campylobact
19	189	7.3	272	2	Q52570 amyoletators

ALIGNMENTS

RESULT	1
Q9M571	PRELIMINARY; PRP; 494 AA.
ID	Q9M571;
AC	Q9M571;
DT	01-OCT-2000 (TREMBL; 15, Last sequence update)
DT	01-MAR-2001 (TREMBL; 16, Last annotation update)
DE	PHOSPHETHANOLAMINE N-METHYLTRANSFERASE (PC 2.1.1.103).
GN	PEAT.
OS	Spinacia oleracea (Spinach).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OC	Caryophyllales; Chenopodiaceae; Spinacia.
OX	NCBI_TaxID:3562;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-SALINIZED LEAF;
RX	MEDLINE-20261526; Pubmed=10799484;
RA	Nuccio M.L., Zieman M.J., Henry S.A., Werthilink E.A., Hanson A.D.;
RT	"Phosphoethanolamine N-methyltransferase from spinach: cDNA cloning by complementation in Schizosaccharomyces pombe and characterization of the recombinant enzyme";
RT	J. Biol. Chem. 275:14095-14101 (2000).
RL	DR AF231633; RAE61950.1; -.
DR	EMBL; InterPro; IPR000551; -.
DR	InterPro; IPR000780; -.
DR	InterPro; IPR001601; -.
KW	Transferase; Methyltransferase.
SQ	SEQUENCE 494 AA; 56361 MW; 7F2537C8E4B8413B CRC64;

Query Match 100.0%; Score 2598; DB 10; Length 494; Best Local Similarity 100.0%; Pred. No. 1.4e-168; Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q9M571

1 MASAMGVQLQEREFVKKWIEHSVDTLVEAMMLDSASLDKVERPEVLSMPPYEGKSV 60

1 MASAMGVQLQEREFVKKWIEHSVDTLVEAMMLDSASLDKVERPEVLSMPPYEGKSV 60

Q9X5Q8

61 LEIIGAGIGRGRFELAERASQVAFDFESVIRKNEESNGHYNVKFICADYPSNISP 120

Q9X5Q9

61 LEIIGAGIGRGRFELAERASQVAFDFESVIRKNEESNGHYNVKFICADYPSNISP 120

Q9Pb2

61 LEIIGAGIGRGRFELAERASQVAFDFESVIRKNEESNGHYNVKFICADYPSNISP 120

QY	121	NSVDIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	180	QY	181	EPFRYTKIFKECHMQDDSGNS'BLSLIGCKC1GAYVSKKQNONQISLWQKVSEDDKGF	240
Db	121	NSVDIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	180	Db	178	EPFRYTKIFKECHMQDDSGNS'BLSLIGCKC1GAYVSKKQNONQISLWQKVSEDDKGF	237
QY	181	EPFRYTKIFKECHMQDDSGNS'BLSLIGCKC1GAYVSKKQNONQISLWQKVSEDDKGF	240	QY	241	QRFLDSSQKFNSLRVERVFGPGYSTGGLETTKEVSKLDLPGQKVLDVCGGDD	300
Db	181	EPFRYTKIFKECHMQDDSGNS'BLSLIGCKC1GAYVSKKQNONQISLWQKVSEDDKGF	240	Db	238	QRFLDNVOYKSSGILRVERVFGPGYSTGGLETTKEVSKLDLPGQKVLDVCGGDD	297
QY	241	QRFLDSSQKFNSLRVERVFGPGYSTGGLETTKEVSKLDLPGQKVLDVCGGDD	300	QY	301	FYMAENYDVVGIDLSINMSFALERSIGLKCAVEEVADCTKKDYPENSEFDVYRDT	360
Db	241	QRFLDSSQKFNSLRVERVFGPGYSTGGLETTKEVSKLDLPGQKVLDVCGGDD	300	Db	301	FYMAENYDVVGIDLSINMSFALERSIGLKCAVEEVADCTKKDYPENSEFDVYRDT	360
QY	301	FYMAENYDVVGIDLSINMSFALERSIGLKCAVEEVADCTKKDYPENSEFDVYRDT	360	QY	361	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	420
Db	301	FYMAENYDVVGIDLSINMSFALERSIGLKCAVEEVADCTKKDYPENSEFDVYRDT	360	Db	361	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	420
QY	361	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	420	QY	421	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	420
Db	361	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	420	Db	418	ILQDAGFVEVIAENRTDQFIVQIQLKEDALEQKDDIDFSEEDYNDIVGKAKLVRTT	480
QY	421	ILQDAGFVEVIAENRTDQFIVQIQLKEDALEQKDDIDFSEEDYNDIVGKAKLVRTT	480	QY	481	EGEQQWGLIFIAKM	493
Db	421	ILQDAGFVEVIAENRTDQFIVQIQLKEDALEQKDDIDFSEEDYNDIVGKAKLVRTT	480	Db	478	SDEQQWGLIFIANK	490
QY	481	EGEQQWGLIFIAKM	494	RESULT	2		
Db	481	EGEQQWGLIFIAKM	494	Q9FR44	PRELIMINARY;	PRT;	491 AA.
AC	Q9FR44			AC	Q9LVH3	PRELIMINARY;	PRT;
DT	01-MAR-2001	(TREMBLrel. 16, Created)		DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		DT	01-MAR-2001	(TREMBLrel. 15, Last sequence update)	
DE	SAM:PHOSPHO-ETHANOLAMINE N-METHYLTRANSFERASE.			DE	358	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	417
GN	NMII.			OS	421	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	477
OS	Arabidopsis thaliana (Mouse-ear cress).			OC	418	ILQDAGFVEVIAENRTDQFIVQIQLKEDALEQKDDIDFSEEDYNDIVGKAKLVRTT	480
OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			OC	481	EGEQQWGLIFIAKM	493
OC	OC			OX	478	SDEQQWGLIFIANK	490
RN	[1]			RN	361	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	420
RP	SEQUENCE FROM N.A.			RP	358	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	417
RC	STRAIN=CV; LANDSPUR ERECTA; TISSUE=STAGE TWO LEAVES;			RC	421	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	477
RX	MEDLINE=20567827; PubMed=11115895;			RX	418	ILQDAGFVEVIAENRTDQFIVQIQLKEDALEQKDDIDFSEEDYNDIVGKAKLVRTT	480
RA	Bolognesi C.P., McGrath P.;			RA	481	EGEQQWGLIFIAKM	493
RT	The Isolation and Characterization in Yeast of a Gene for Arabidopsis S-Adenosylmethionine:Phospho-Ethanolamine N-Methyltransferase.;"			RA	478	SDEQQWGLIFIANK	490
RT	Plant Physiol. 124:1800-1813 (2000).			RA	361	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	420
RL	EMBL: AF197940; AAG41121.1; -.			RA	358	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	417
KW	Transferase; Methyltransferase.			RA	421	ILHQDKPALFSFKWKLPGSKVLSIDYCKSAGTPEAFAAYIQRQYDIDVKAQGM	477
SQ	SEQUENCE 491 AA; 56102 MW; DA4404EBED3FA8D5 CRC64;			RA	418	ILQDAGFVEVIAENRTDQFIVQIQLKEDALEQKDDIDFSEEDYNDIVGKAKLVRTT	480
Query	Match	81.0%	Score 2105.5; DB 10; Length 491;	RESULT	3		
Best	Local Similarity	78.9%	Pred. No. 4e-135;	Q9LVH3	Q9LVH3	PRELIMINARY;	PRT;
Matches	389;	Conservative	55; Mismatches 46; Indels 3; Gaps 1;	AC	Q9LVH3	PRELIMINARY;	PRT;
QY	1	MAASAMGVQLQEREVFKWYIHEHSVDTVEAMMLDSQASDLDKVERPEVLMLPPYEGKSV	60	DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)	
Db	1	MAAS--YEERDIQKWIHEHSADLTVEMMLDSRASDLDEKEERPEVLMLPPYEGKSV	57	DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	
QY	61	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120	OS	Arabidopsis thaliana (Mouse-ear cress);		
Db	58	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120	OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
QY	121	NSVDIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	180	OX	OC		
QY	121	NSVDIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	180	OX	OX		
Db	118	GSLDLIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	177	OX	OX		
Query	Match	80.5%	Score 2093; DB 10; Length 498;	Query	1	MAASAMGVQLQEREVFKWYIHEHSVDTVEAMMLDSQASDLDKVERPEVLMLPPYEGKSV	60
Best	Local Similarity	78.0%	Pred. No. 2.9e-14;	Match	1	MAASAMGVQLQEREVFKWYIHEHSVDTVEAMMLDSQASDLDKVERPEVLMLPPYEGKSV	60
Matches	390;	Conservative	54; Mismatches 46; Indels 10; Gaps 2;	Q9LVH3	Q9LVH3	PRELIMINARY;	PRT;
QY	1	MAASAMGVQLQEREVFKWYIHEHSVDTVEAMMLDSQASDLDKVERPEVLMLPPYEGKSV	60	Db	1	MAAS--YEERDIQKWIHEHSADLTVEMMLDSRASDLDEKEERPEVLMLPPYEGKSV	57
Db	1	MAAS--YEERDIQKWIHEHSADLTVEMMLDSRASDLDEKEERPEVLMLPPYEGKSV	57	Db	1	MAAS--YEERDIQKWIHEHSADLTVEMMLDSRASDLDEKEERPEVLMLPPYEGKSV	57
QY	61	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120	RA	61	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120
Db	58	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120	RA	58	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	117
QY	121	NSVDIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	180	RA	61	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120
Db	118	GSLDLIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	177	RA	58	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	117
Query	Match	80.5%	Score 2093; DB 10; Length 498;	Query	1	MAASAMGVQLQEREVFKWYIHEHSVDTVEAMMLDSQASDLDKVERPEVLMLPPYEGKSV	60
Best	Local Similarity	78.0%	Pred. No. 2.9e-14;	Match	1	MAASAMGVQLQEREVFKWYIHEHSVDTVEAMMLDSQASDLDKVERPEVLMLPPYEGKSV	60
Matches	390;	Conservative	54; Mismatches 46; Indels 10; Gaps 2;	Q9LVH3	Q9LVH3	PRELIMINARY;	PRT;
QY	1	MAASAMGVQLQEREVFKWYIHEHSVDTVEAMMLDSQASDLDKVERPEVLMLPPYEGKSV	60	Db	1	MAAS--YEERDIQKWIHEHSADLTVEMMLDSRASDLDEKEERPEVLMLPPYEGKSV	57
Db	1	MAAS--YEERDIQKWIHEHSADLTVEMMLDSRASDLDEKEERPEVLMLPPYEGKSV	57	Db	1	MAAS--YEERDIQKWIHEHSADLTVEMMLDSRASDLDEKEERPEVLMLPPYEGKSV	57
QY	61	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120	RA	61	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120
Db	58	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120	RA	58	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	117
QY	121	NSVDIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	180	RA	61	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	120
Db	118	GSLDLIFSNWLMLYLSDEVERLVERMLKWLKPGYIFFRESCFHQSQGDHKRKSNPHTYR	177	RA	58	LELGAGIGRFGELAKASQVIALDFIESVKKNESINGHYKVNKFMCADYVPSLNISP	117

SO	SEQUENCE	374 AA;	42656 MW;	318D85E0311C0C47 CRC64;
QY	181 EPRFYTKI-----FKECHMODDSGNSEUSLIGCKCIGAVKSKKKNQNQTSWLMWKVD	233		
	: : : : : : : : : : :			
Db	178 EPRFYTKIDGETDMKVFOECQTRDAAGNSFELSMIGCKCIGAVKNNQNQTCWIKVUS	237	Query Match	49.6%; Score 1287.5; DB 10; Length 374;
			Best Local Similarity	66.4%; Pred No. 9.6e-80;
			Matches	243; Conservative 36; Mismatches 28; Indels 59; Gaps 2;
QY	234 SEDDKGFORFLDSQYKFNSTIRYERVFGPGVUSTGLETTEKFVSKLDRKGQVKIDVG	293		
	: : : : : : : : : : :			
Db	238 SENDRGFQRFLDNVQYKSSGILRIVERYERVFGPGVUSTGLETTEKFVSKLDRKGQVKIDVG	297		
			Query	187 KIRKECHMODDSGNSEUSLIGCKCIGAVKSKKKNQNQTSWLMWKVDSEDDKFORFLDS
				: : : : : : : : : :
QY	294 CGIGGDFYMAENYDVEWVGDLSINMSFALERSIGLKCAVEFEVADCTKRDYPENSFD	353	246	
	: : : : : : : : : :			
Db	298 CGIGGDFYMAEKFHDVHGVIDLSVNMSFALERAIGLCSFEVADCTKRDYPENSFD	357		
			Db	68 VQYKSGGLRVERVFGPGVUSTGGL-----ETKE 276
QY	354 VIYSROTILHQDKPALFRSHKWLKGKVLISDCKSAGTPSAEFAAYRQRGTDLH	413		
	: : : : : : : : : :			
Db	358 VIYSROTILHQDKPALFRSHKWLKGKVLISDCKSAGTPSAEFAAYRQRGTDLH	417	Query	277 FVSKLDRKGQVKIDVGCGIGGDFYMAENYDVEWVGDLSINMSFALERSIGLKCAVE
				: : : : : : : : :
QY	414 VYAKGKMLKDGAFVETTAENRDTQFQVQLQKELDALEQEKDFTDFSEEDYNDIVGK	473	336	
	: : : : : : : : :			
Db	418 VQAYGOMLKDAGFTDVIADRTDQFMQVLSKRELDVREKEKERFISDFSKEDYDDIVGK	477		
			Db	128 FVAKMDLKGQVKIDVGCGIGGDFYMAENFDVHVGVIDLSVNMSFALERAIGLCSVE
QY	474 AKLVRTEGEQWQGLFLAK 493			187 337 FEVADCTKRDYPENSFDVYISROTILHQDKPALFRSHKWLKGKVLISDCKSACTP
				: : : : : : : : :
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;			: : : : : : : :
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;			: : : : : : :
OC	Brassicales; Brassicaceae; Arabidopsis.			: : : : : : :
OX	NCBI_TaxID=3702;			: : : : : : :
RN	SEQUENCE FROM N.A.			: : : : : : :
RP	Q9LP63: 01-OCT-2000 (TREMBL). 15, Created)			: : : : : : :
RP	Q9LP63: 01-OCT-2000 (TREMBL). 15, Last sequence update)			: : : : : : :
DT	01-MAR-2001 (TREMBL). 16, Last annotation update)			: : : : : : :
DE	TIN15 23.			: : : : : : :
OS	Arabidopsis thaliana (Mouse-ear cress).			: : : : : : :
OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;			: : : : : : :
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;			: : : : : : :
OC	Brassicales; Brassicaceae; Arabidopsis.			: : : : : : :
OX	NCBI_TaxID=3702;			: : : : : : :
RN	"Genomic sequence for Arabidopsis thaliana BAC TIN15 from chromosome			: : : : : : :
RP	I."			: : : : : : :
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			: : : : : : :
RN	[2]			: : : : : : :
RP	SEQUENCE FROM N.A.			: : : : : : :
RA	Ecker J.R.;			: : : : : : :
RA	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			: : : : : : :
RN	[3]			: : : : : : :
RP	SEQUENCE FROM N.A.			: : : : : : :
RA	Ecker J.R.;			: : : : : : :
RA	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			: : : : : : :
RN	[4]			: : : : : : :
RP	SEQUENCE FROM N.A.			: : : : : : :
RA	Chen P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,			: : : : : : :
RA	Khan S., Kim C., Alttaifi H., Bel B., Chin C., Chiou J., Choi E.,			: : : : : : :
RA	Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,			: : : : : : :
RA	Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N., Theologis J.,			: : : : : : :
RA	Theologis J., Ecker J., Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			: : : : : : :
DR	EMBL; AC020889; AAFT9705.1; -.			: : : : : : :
DR	INTERPRO; IPR00051; -.			: : : : : : :
DR	INTERPRO; IPR01601; -.			: : : : : : :

RA	Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Denz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavei A., Toiumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;	DR	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.	
RA	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.	DR	EMBL: AC020889; AAF7904.1; -.	
DR	InterPro: IPR00051; -.	DR	InterPro: IPR00039; -.	
DR	InterPro: IPR000780; -.	DR	InterPro: IPR001601; -.	
SQ	SEQUENCE 180 AA; 20472 MW; AA0FDEF2DD27E556 CRC64;	KW	Pfan: P101209; Ubile methyltran; 1.	
Query	Match	29.5%; Score 767.5; DB 10; Length 180;	SEQUENCE 437 AA; 49769 MW; 6675E262F627D08B CRC64;	
Best Local Similarity	75.4%; Pred. No. 7e-45;	Best Local Similarity	32.6%; Pred. No. 4.6e-26;	
Matches	144; Conservative 19; Mismatches 17; Indels 11; Gaps 1;	Matches	127; Conservative 70; Mismatches 156; Indels 37; Gaps 10;	
QY	20 IEHSVDLTVTEAMMDSQASDLDKVERPEVLSMLPYRGKSVBLGAGIGRGRFELAERAS 79	QY	121 NSVDIFSNWMLWLSDEVERVERLVERMLKWLKP-----GGYIFFRSCFHOSGDHKKR 173	
Db	1 MEHSSDLTVEAMMDSKASDLKVERPEVLSMLPYRGKSVBLGAGIGRGRFELAOKAG 60	Db	64 NADVLIFNNALSOQITNADL----LTDFLKNATNATAIGGTVIRED-LKCSDRKRQV 116	
QY	80 QVIALDFEVSKVNNESNGHKNVKNCADYPSNPSUNISPNVDIFSNWMLWLSDEE 139	QY	174 SNPHTYRPRPFYKIKKCHMDDGSNYESLJLGCKI---GAYVSKKKKKNQNOISWIM-- 229	
Db	61 EVIALDFEVSKVNNESNGHKNVKNCADYPSNPSUNISPNVDIFSNWMLWLSDEE 120	Db	117 ARLJDY-----FDVFRTTDSGNNNTGGLDLYTVQDVEHSNYE---QNLDFLFVF 163	
QY	140 VERLVERMLKWLKPQGYIFFRSCFHOSGDKSKRKNPKNKADMVSPDJKIKDGSIDLIFSNWMLWLSDE 199	QY	230 :QKV--DSEDDKGFORLDDSSQYKFNSLRILVERVFGPGVNSTGGLETTKERSVSL-DLK 284	
Db	121 VELMAERMGWYKPGGYIFFRSCFHOSGDKSKRKNPKNKADMVSPDJKIKDGSIDLIFSNWMLWLSDE 169	Db	164 RKKVFAPTTATIFRDLKQYQNTNGIDAYEVMMEFGVNTSPGGYDENLKIIRRDFK 223	
QY	200 NSYELSLIGCK 210	QY	285 PGOKVLDVGCIGGGDFWMAENDVVEVGIDISINNTSFLERSIGK-CAVEFEADCT 343	
Db	170 QSFDLTFLK 180	Db	224 PGQTMLDIDGVIGGARGARQVADBERGVHVGIDLSSNMLAIALBLRHEEKDSRKYSDTAL 283	
RESULT	6	QY	344 KKDPYENPSFDVITSRDTLHDKPRAFLKQYQNTNGIDAYEVMMEFGVNTSPGGYDENLKIIRRDFK 223	
ID	Q22993	PRELIMINARY;	Db	284 VIOFEDNSFDYFVFSRDCIQHIDPDTKESRRIKKALPKPGKVLITMGKGYGEOSDKFTY 343
AC	Q22993;	PRY;	QY	404 IRQRGYDIDHVKAYGKMKDAGEVENIAENRPOFIQYLOKEIDALRQEKDIDPFDSEE 463
DT	01-NOV-1996 (Tremblrel. 01, Created)	Db	344 VAQRAYFLKLNLKELADTANKTGIVNQVTEMMPRFKEILLEERGHLEQNEABEMSKFTQ 403	
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)	QY	464 DYNDIVDGWKKAKLYRTFEGEQQNGFLAKK 493	
DE	01-JUN-2000 (Tremblrel. 14, Last annotation update)	Db	404 ERDSLISGWTDLKGYIEKDNNHNNFLAQK 433	
GN	PS4DII-1.	RESULT	7	
OS	Ceenorhabditis elegans.	Q23552	Q23552	
OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;	ID	Q23552;	
OC	Rhabditidae; Peioderinae; Caenorhabditis.	AC	Q23552;	
OX	NCBI_TaxID=6239;	DT	01-NOV-1996 (Tremblrel. 01, Created)	
RN	[1] SQUENCE FROM N.A.	DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)	
RC	STRAIN=BRISTOL NZ;	DE	CODED FOR BY C. ELEGANS CDNA YK92B11.3.	
RX	MEDLINE=94150718; PubMed=7906398;	GN	ZK6222.3.	
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,	OC	Ceenorhabditis elegans.	
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	OC	Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea;	
RA	Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,	OC	Rhabditidae; Peioderinae; Caenorhabditis.	
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,	OC	NCBI_TaxID=6239;	
RA	Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,	OX	[1] SQUENCE FROM N.A.	
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,	OX	MEDLINE=94150718; PubMed=7906398;	
RA	Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,	RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,	
RA	Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,	RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	
RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,	RA	Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,	
RA	Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,	RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,	
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans." / Nature 368:32-38(1994).	RA	Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,	
RT	[2] SEQUENCE FROM N.A.	RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,	
RA	SEQUENCE FROM N.A.	RA	Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,	
RA	STRAIN=BRISTOL NZ;	RA	Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,	
RA	Pauley A., Gattung S.;	RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,	
RA	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.	RA	Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,	
RA	[3] SEQUENCE FROM N.A.	RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans" / Nature 368:32-38(1994).	
RC	STRAIN=BRISTOL NZ;	RL	[2] Nature 368:32-38(1994).	
RA	Waterston R.;	RL		

RP	SEQUENCE FROM N.A.	SQ	SEQUENCE	565 AA:	64718 MW;	856FB62BC66A149C CRC64;	
RA	Leimbach D.;	Query Match	8.6%;	Score 223;	DB 2;	Length 565;	
RL	Submitted (Nov-1995) to the EMBL/GenBank/DBJ databases.	Best Local Similarity	22.1%;	Pred. No. 3.4e-07;			
RN	[3]	Matches	113;	Conservative	76;	Mismatches 220;	
RA	Waterson R.;	Indels	73;	Gaps	17;		
RL	Submitted (Nov-1995) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; U39998; AAAB1102.1; -.	QY	12 REVFKKYWIEHSVSDLTVEAMMLDSQASLDLKVPERPEVLSMLPYEGSYLELGAGIGRFT 71	41 RANKFSFDWYKSDKPDNTSMMLNHSABLESSDRRADIASLPLHNDKVVDIGAGIGRFT 100	QY	58 KSVLELGAGIGRFTGELAEKASOVIADFIESVIKKNES---INGIYKNT---KFMC 108	
DR	InterPro; IPR00051; -.	QY	72 GELEAKASQVIAFLDFISVIKNEESINGHYKAVKFMGADVIPSINSPNSDITISNWL 131	101 TVLAETAKWNLSTDFISFIKKNQVRNHWLNGHNYNQYQDAV--GLKHESSNDLVEFNWL 158	QY	80 ETVLAATGTFHSVRLLEGEETVSADGSPOMLAKAFNSGLAYNGLRWNADWRWL 139	
DR	SEQUENCE 495 AA; 57262 MW;	Db	109 ADYTSPIINSNSVDTIIFSNWILMYSDEVERLVRMLKWLPGSYIWERESCRFQSG 168	140 RDVHGEYDAI-----ICLGNNSFTHLSERDRRKTLAEFYAMLKHDGLVLIIDQRNDSIL 193	QY	169 DHKRKNTHY-----REP-----RF-YTKIKECHKDDSG---NSYELSL-- 206	
KW	Query Match 17.3%; Score 449.5; DB 5; Length 495; Best Local Similarity 28.6%; Pred. No. 1.2e-22; Matches 137; Conservative 74; Mismatches 195; Indels 73; Gaps 17;	Db	194 DPGFSKTYVYAGEDSYAEPDIDGLARFKT-----EPDKSIEFFLNMPYPLRDYM 246	207 -----LGCKCIGAYVSKKKNNQNIQSWLWQKVDSEDDKGFQRFLDSSQYK----- 250	Db	247 RRLMREVGFORIDTYGD-----FOEYGEDPFDYIHAESYRTEDEFDMYS 295	
QY	132 LMWLSDDEVERLVRMLKWLPGGYIFREFSCPHQS-GDHKRKS-----NPTHYREPR 183	QY	251 -----FNSLIR--YERYFGPGVYSTGGLETTEKFVFS-----KLDLPG 286	Db	296 NAVHTARDYNSEDADNFYVHWGNDIHWGLYQTPOEDIATASERTVORMAGKVDISPE 355	QY	287 QKVLDSGGIGGSDFYMAENYDVEWGLDS - INMISFALESRSIGKCAVEFEVADTK 344
Db	159 MMYLSDDETFVFNCWHLRSHGIVLRESCPSTGSKAKSMHDTANANPHTYRESS 218	QY	356 TRILDGAGYGGARYLARTYQCHVTCINLSEVENORNRTRAEGLHLI-EVTDGSF 413	Db	414 ELDPYODNAFDVWWSOSFLHSGLSDRSRVEVTRVLKPKGSVLFDTMASBKKNLGP 473	QY	345 KD-YPENSFDVYTSRDTILHDKPALKFPLRSFHKWLKPGKVLISDYCKSAGTPSAFAA 402
QY	184 FVTKTFKCHMODOGSNSYELSLIGCKCIGAYVSKKKNNQNIQSWLWQKVDSEDDKGFQRFLDSSQYK----- 240	Db	403 YIRQGYW-LHDVKAYGKMLKDAGFVEVIAENRTDQF1QV1QKELDALEQKDDF1DDFS 461	Db	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	462 EEDYNDLVDGWKAKLVRITGEBOGWLFTAK 492
Db	219 LYINLRLRARRYDWDKLNWRFNQWQSCSVPTYIKRSNNWQHWAEXVPAEDAKTSF 278	QY	534 EERAHMKTGLRWWQAGNGGSLAWGIHAR 564	Db	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
QY	241 QRFLD-----SSQYENIYERYFGPGVYSTGGLETTEKFVFS-----KLDLPG 286	Db	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
Db	279 NEVLELTKNTWQNEQDAKLDDE-----VV-----WTDKVFESSALTSPLSNSTFLY 328	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
QY	288 --KVLWDGCGIGGGFVMAENYDVEWGLDSINMISFALESRSIGKCAVEFEVADTK 337	Db	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
Db	329 TPPTVSPYCHINA - HTLAETANAVNVRNTTEIPEYYRTSLTSNKLQDORVRFQWNQSLT 386	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
QY	338 -EVADCTKDYFENSFDVYTSRDTILHDKPALKFPLRSFHKWLKPGKVLISDYCKSAGTP 396	Db	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
Db	387 DSVTYWQKD--ALFDVFATEFLSPVDE--TIRQLPNWMSDGAKEFILEPDEVN- 439	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
QY	397 SABFAAYTQRGQYDLDHVAKYGRMLKDAGFVEVIAENRTDQTOVLOKELDALEQKDD 455	Db	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533	QY	474 ILDRHILDSLGSQFYRKELTRIGLQNIEFEDOLSEYLPVHIGRVLLEVLESRENELAGFIG 533
Db	440 EADMKRIOELGYL-----KSFTDV----TDOQIEAQDQYFKQHEQLRDE 481	RESULT	9	AC	Q41586	PRELIMINARY;	
RESULT	8	ID	Q41586	AC	Q41586	PRELIMINARY;	
09KJ20	09KJ20	AC	Q41586	AC	Q41586	PRELIMINARY;	
AC	PRELIMINARY;	PRT:	565 AA.	PRT:	363 AA.		
DT	01-OCT-2000 (TREMBREL 15, Created)	DT	01-NOV-1996 (TREMBREL 01, Created)	DT	01-FEB-1997 (TREMBREL 02, Last sequence update)		
DT	01-OCT-2000 (TREMBREL 15, Last sequence update)	DT	01-JUN-2000 (TREMBREL 14, Last annotation update)	DT	01-JUN-2000 (TREMBREL 14, Last annotation update)		
DT	01-MAR-2001 (TREMBREL 16, Last annotation update)	DE	DELTAA-24-STEROL METHYLTRANSFERASE.	DE	DELTAA-24-STEROL METHYLTRANSFERASE.		
DE	GLUCINE-SARCOINE-DIMETHYLGLYCINE METHYLTRANSFERASE.	GN	TA-MT	GN	TA-MT		
OS	Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Pseudonocardineae; Pseudonocardiaaceae;	OS	Triticum aestivum (Wheat)	OS	Triticum aestivum (Wheat)		
OC	Actinomycetales; Pseudonocardineae; Pseudonocardiaaceae;	OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Actinomycetospora; Actinomycota; Actinomycetomycetidae; Actinomycetomycetidae;	OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae;	OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae;		
OC	Actinomycetospora halophilica.	OX	Triticum	OX	Triticum		
OX	[1]	NCBI_TAXID=4565;	NCBI_TAXID=4565;	NCBI_TAXID=4565;	NCBI_TAXID=4565;		
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.		
RN	RA	RA	Subramanian K., Ueng P.-P.;	RA	Subramanian K., Ueng P.-P.;		
RN	RA	RA	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.	RA	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.		
RN	RA	RA	EMBL; U50754; AAB37691;	RA	EMBL; U50754; AAB37691;		
RN	RA	RA	Mende1; 10873; Triae; 1138; 10873.	RA	Mende1; 10873; Triae; 1138; 10873.		
RN	RA	RA	InterPro; IPR00051; -.	RA	InterPro; IPR00051; -.		
RN	RA	RA	InterPro; IPR001601; -.	RA	InterPro; IPR001601; -.		
RN	RA	RA	Transferase; Methyltransferase.	RA	Transferase; Methyltransferase.		
RN	RA	RA	Sequence 363 AA; 41603 MW; 7F209945D6A62C75 CRC64;	RA	Sequence 363 AA; 41603 MW; 7F209945D6A62C75 CRC64;		
RT	Query Match 8.0%; Score 207; DB 10; Length 363;	RT	Query Match 8.6%; Score 223; DB 2; Length 565;	RT	Query Match 8.6%; Score 223; DB 2; Length 565;		
RL	Best Local Similarity 28.6%; Pred. No. 2.2e-06;	RL	Best Local Similarity 22.1%; Pred. No. 3.4e-07;	RL	Best Local Similarity 22.1%; Pred. No. 3.4e-07;		
DR	Matches 68; Conservative 38; Mismatches 88; Indels 44; Gaps 8;	DR	Matches 113; Conservative 76; Mismatches 220; Indels 102; Gaps 17;	DR	Matches 113; Conservative 76; Mismatches 220; Indels 102; Gaps 17;		

DR	09KJ21	SEQUENCE	278 AA;	3046 MW;	9804BC2024BD85C1	CRC64;
SQ						
Query Match	7.7%;	Score	199;	DB 2;	Length	278;
Best Local Similarity	26.6%;	Pred.	No. 5.	2e-06;		
Matches	62;	Conservative	48;	Mismatches	101;	Indels 22;
						Gaps 8;
Db	274	TKEFVSKLDLPGOKVLDVGCGIGGGDFYMAENYDVVGIDLISINMISFA---LERSIG	330			
	52	TEMTERIEVPGFPGVLDIGCTGAPAVOLARATGEVGITISPEOVRATAHAERE-G	110			
QY	331	LKCAVEFEVADCTKK-DYPPENSFDVYISRDTLHQDKPALERSFIHKWLKGKGK---V	384			
	111	VAERVFPRCADASAELEPPADSFDAWVFFESIHLPDRLTALLRAAEVLRPGGRLATDV	170			
Db	385	LISDICKSGATPSAEPAYIQRGVDLHDVKAYGKMKDAGFEV---IAENRTDFOIQ	440			
QY	171	LHNDETSPAAESLDHAYTPLVGEPMR-LSDYPPILRQARIWVPCERDIBLTVGRTLE	229			
Db	441	VLOKELDALEQEKDDFDSEEDYNDIVDGSKAKLVRTRTEGQDWLFTARK	493			
QY	230	CMHRTLD--ENRERFVERYSE---LVDQFSTAVPLDAVEFGYIVTAA	275			
RESULT	13					
082720		PRELIMINARY;	PRT;	346 AA.		
ID	082720					
AC	082720;					
DT	01-NOV-1998	(TREMBLrel. 08, Created)				
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)				
DE	01-NOV-2000	(TREMBLrel. 14, Last annotation update)				
OS	Nicotiana tabacum	(Common tobacco)				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.					
OC	NCBI_TaxID=4097;					
OX	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=XANTHI	S16;				
RY	MEDLINE=98A17432;	PUBMed=9746350;				
RA	Bouvier-Nave P., Huiselstein T., Benveniste P.:					
RT	"Two families of sterol methyltransferases are involved in the first and the second methylation steps of plant sterol biosynthesis.;"					
RT	and Eur. J. Biochem. 256:88-96 (1998).					
DR	EMBL; U81312; AAC34931.1; -;					
DR	Mende1; 33290; Nicta.1138; 33290.					
DR	InterPro; IPR000051; -;					
KW	Transferase; Methyltransferase.					
SQ	SEQUENCE	346 AA;	38871 MW;	E7A3F95349D94A4	CRC64;	
Query Match	7.5%;	Score	196;	DB 10;	Length	346;
Best Local Similarity	34.4%;	Pred.	No. 1.	1e-05;		
Matches	55;	Conservative	27;	Mismatches	68;	Indels 10;
						Gaps 5;
RESULT	15					
043445		PRELIMINARY;	PRT;	367 AA.		
ID	043445					
AC	043445;					
DT	01-NOV-1996	(TREMBLrel. 01, Created)				
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)				
DE	S-ADENOSYL-L-METHIONINE:DELTA24-STEROL-C- METHYLTRANSFERASE.					
OS	Glycine max (Soybean).					
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.					
OC	NCBI_TaxID=3847;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CV; WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYL;					
RY	MEDLINE=96193190; PubMed=8621604;					
RA	Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.;					
RT	"Identification and characterization of an S-adenosyl-L-methionine: delta 24-sterol-C-methyltransferase cDNA from soybean.;"					
RT	J. Biol. Chem. 271:9384-9389(1996).					
DR	215 NNEEHNRKAEIELGNGLPLPEVRLTQCLEAAKQAGF-EVV	253				
RESULT	14					
09KJ21	SEQUENCE FROM N.A.					
09KJ21	PRELIMINARY;	PRT;	279 AA.			
DR	SEQUENCE FROM N.A.					
DR	STRAIN=CV; WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYL;					
DR	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.					

DR EMBL; U43683; AA004057; 1; -.
 DR Mendel; 8195; Glyma; 1138; 8195.
 DR InterPro; IPR00051; -.
 KW Transferase; Methyltransferase.
 SQ SEQUENCE 367 AA; 41518 MW; B3EBF8D2F0B22FB4 CRC64;

Query Match 7.4%; Score 191; DB 10; Length 367;
 Best Local Similarity 22.5%; pred. No. 2.7e 10;
 Matches 81; Conservative 48; Mismatches 119; Indels 112; Gaps 12;

DB 54 HVCYGGQEEERKANYTDMVNUKYDVLTSYFPGWGSFPHFAPRWKGESLIESIKRHEFL 113
OV 281 ---LDLPGKVKLUDVKGIGGGDFEYANNVYEVVGDLSNMTIPEA---FERSIGLICAV 335

DB 114 PQLQGLRPGQKVYLDVGCGGGPLREISRFSSSTITGLNNNNQITRGKELNTRAGDKTC 173
 QY 336 EFEVADCTKQYOPENSDVYISRTDLHIDDKPALKPFRSHFHLWKLGGKVYLSDYCKSAG- 394

QY 395 --TPSAEEFAAYIQRQYDLDHVAKAGK--MLKDAVGVENTAENR----- 434
 :
 DB 234 DPONPEIOKIKRATIEGDLGDRDILRKACLLKAGF-EIWKEVLDLAVSPPLPYRLPD 292

Db	QY	435	-----TOFIVQVQKEDDALEBKKDDFTDDESEBDYDIVDCKWAKI	476
293	KSHFSLSSFRITAVGRLFTKMKVVL-ENVGLAOKGSLVQDFLEKAAGLVEGGKREI	350		

Search completed: September 20, 2001, 16:21:05
Job time: 172 sec

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Job time: 172 sec